



# Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Oct 15, 2019 – 11:27 PM EDT

PDB ID : 4A7L  
EMDB ID: : EMD-1989  
Title : Structure of the Actin-Tropomyosin-Myosin Complex (rigor ATM 1)  
Authors : Behrmann, E.; Mueller, M.; Penczek, P.A.; Mannherz, H.G.; Manstein, D.J.;  
Raunser, S.  
Deposited on : 2011-11-14  
Resolution : 8.10 Å(reported)  
Based on PDB ID : 3MFP, 1LKK

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report  
for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

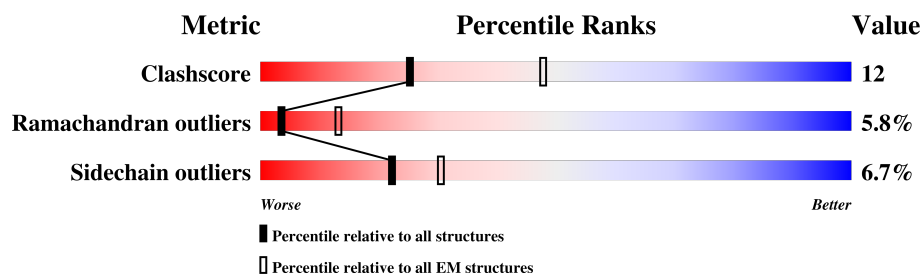
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 8.10 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	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

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  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	375	
1	D	375	
1	E	375	
1	F	375	
1	I	375	
2	B	136	
2	H	136	
3	C	697	
3	G	697	

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	J	697	<div><div></div><div>77%</div><div>18%</div><div>• •</div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 33500 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 ACTIN, ALPHA SKELETON MUSCLE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	375	Total	C	N	O	S	0	0
			2934	1855	493	565	21		
1	D	375	Total	C	N	O	S	0	0
			2934	1855	493	565	21		
1	E	375	Total	C	N	O	S	0	0
			2934	1855	493	565	21		
1	F	375	Total	C	N	O	S	0	0
			2934	1855	493	565	21		
1	I	375	Total	C	N	O	S	0	0
			2934	1855	493	565	21		

- Molecule 2 is a protein called TROPOMYOSIN 1 ALPHA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	136	Total	C	N	O	S	0	0
			1104	673	189	239	3		
2	H	136	Total	C	N	O	S	0	0
			1104	673	189	239	3		

- Molecule 3 is a protein called MYOSIN IE HEAVY CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	689	Total	C	N	O	S	0	0
			5494	3469	946	1048	31		
3	G	689	Total	C	N	O	S	0	0
			5494	3469	946	1048	31		
3	J	689	Total	C	N	O	S	0	0
			5494	3469	946	1048	31		

There are 9 discrepancies between the modelled and reference sequences:

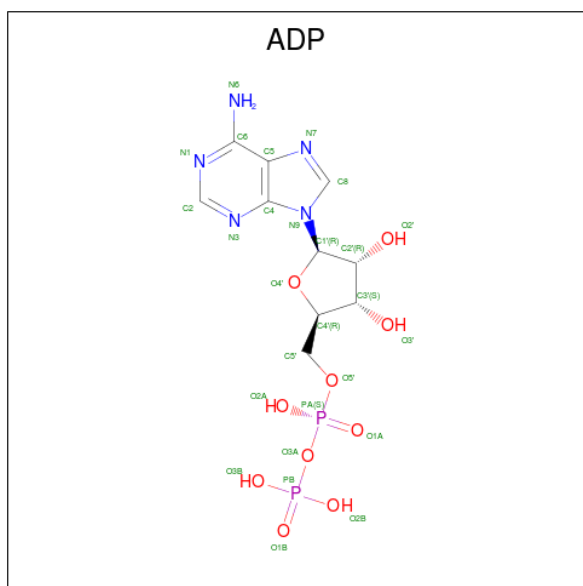
Chain	Residue	Modelled	Actual	Comment	Reference
C	77	MET	ILE	conflict	UNP Q03479

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	215	ASP	ASN	conflict	UNP Q03479
C	334	GLU	SER	engineered mutation	UNP Q03479
G	77	MET	ILE	conflict	UNP Q03479
G	215	ASP	ASN	conflict	UNP Q03479
G	334	GLU	SER	engineered mutation	UNP Q03479
J	77	MET	ILE	conflict	UNP Q03479
J	215	ASP	ASN	conflict	UNP Q03479
J	334	GLU	SER	engineered mutation	UNP Q03479

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	F	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	I	1	Total	C	N	O	P	0
			27	10	5	10	2	

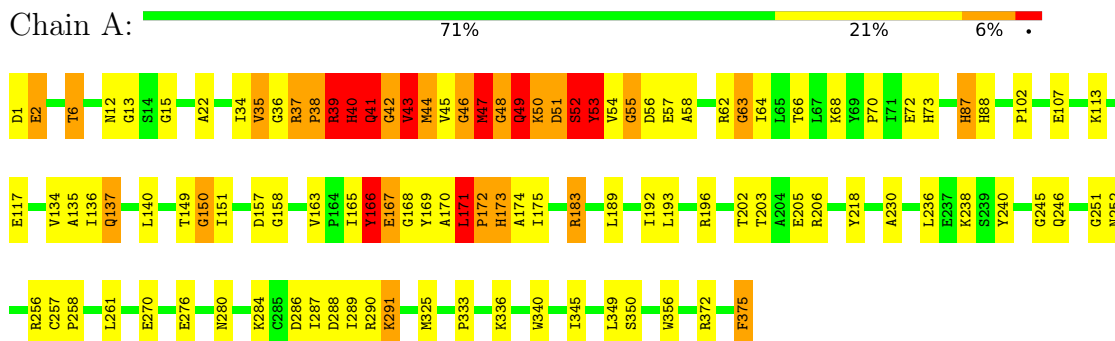
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
5	I	1	Total 1	Ca 1	0
5	A	1	Total 1	Ca 1	0
5	D	1	Total 1	Ca 1	0
5	F	1	Total 1	Ca 1	0
5	E	1	Total 1	Ca 1	0

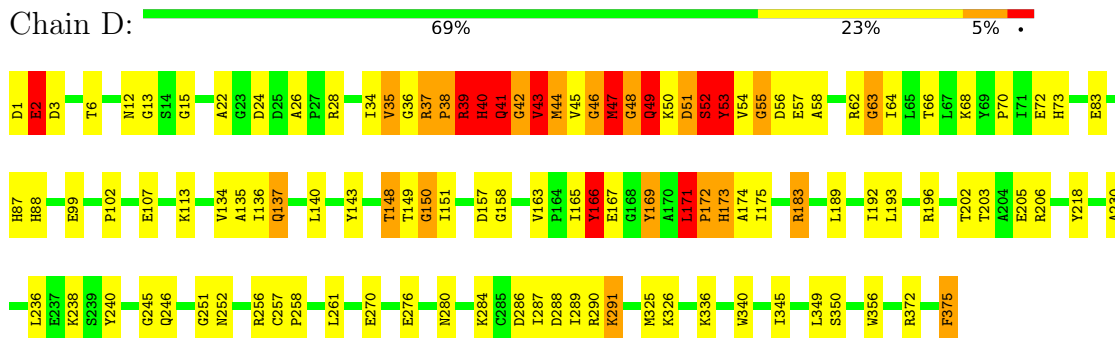
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

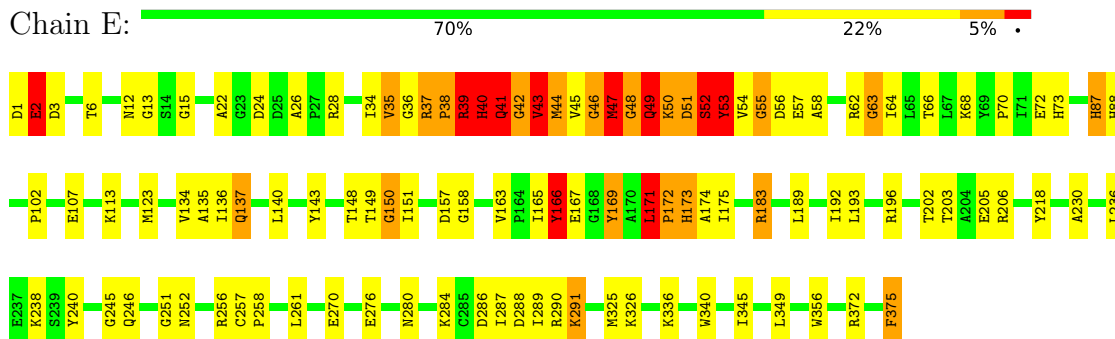
- Molecule 1: ACTIN, ALPHA SKELETON MUSCLE



- Molecule 1: ACTIN, ALPHA SKELETON MUSCLE

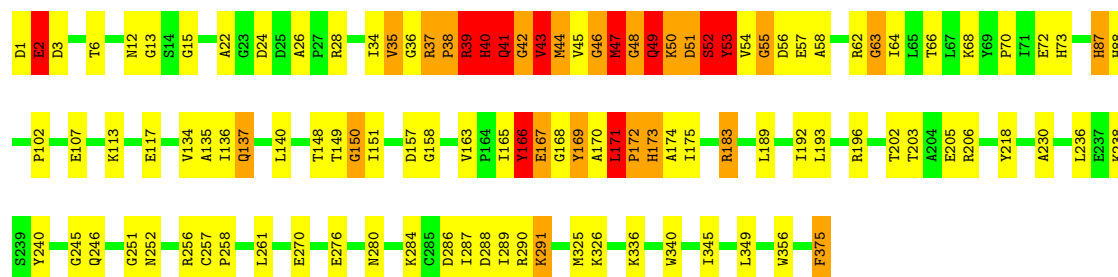


- Molecule 1: ACTIN, ALPHA SKELETON MUSCLE



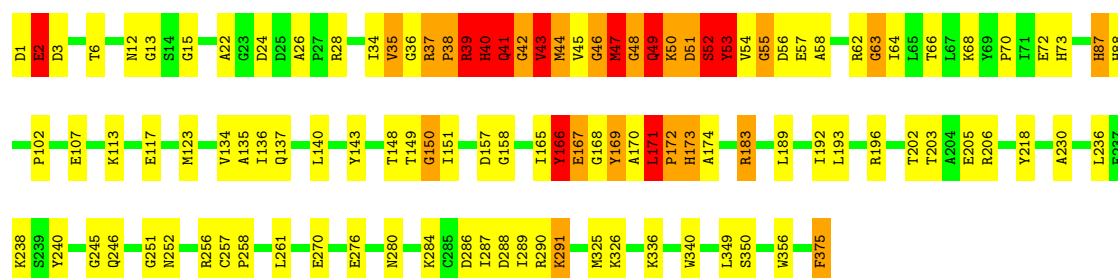
- Molecule 1: ACTIN, ALPHA SKELETON MUSCLE

Chain F:  70% 22% 6%



- Molecule 1: ACTIN, ALPHA SKELETON MUSCLE

Chain I:  70% 22% 5%



- Molecule 2: TROPOMYOSIN 1 ALPHA

Chain B:  97%




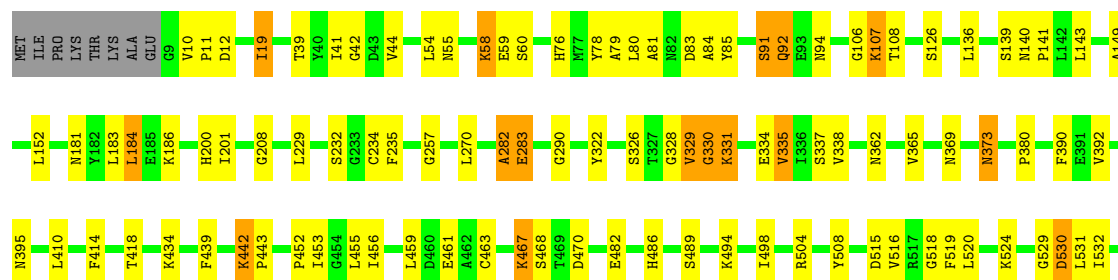
- Molecule 2: TROPOMYOSIN 1 ALPHA

Chain H:  96%



- Molecule 3: MYOSIN IE HEAVY CHAIN

Chain C:  78% 17%







K674	G518	N369	L143	MET
T675	F519	N373	A149	ILE
V677	L520	P380	L152	P80
F678	K524	F390	N181	LVS
L679	G529	E391	Y182	TTR
	D530	V392	L183	LVS
	L531	N395	L184	ALA
T684	L532	L410	E185	GLU
	F547	F414	K186	G9
L684	F548	L417	H200	P11
P697	F549	T418	T201	D12
	T550	S421	G208	T19
	R551	K434	A223	T39
	K557	F439	P224	Y40
	R558	K442	L229	I41
	P559	P443	G232	G42
	E560	P452	E235	D43
	L573	I453	G257	V44
	E601	G454	L270	L54
	R605	I456	A282	N55
	H606	L459	E283	K58
	Q607	D460	E286	E59
		E461	Q287	S60
		A462	R288	H76
	Y610	C463	T289	H77
		K467	G290	Y78
	R620	S468	R323	A79
	R621	T469	S326	L80
	G622	E482	T327	A81
	G623	H486	G328	N82
	F624	S489	V329	D83
	A625	K494	C330	A84
	G626	R496	K331	Y85
	R627	Y508	E334	S91
	L628		V335	Q92
	F629		I336	E93
	Y630		S337	N94
	F633		V338	G106
	G634		N362	K107
	N635		D515	T108
	R636		V516	E109
	T637		T517	A110
	G638			S111
	M639			S126
				L136
				S139
				N140
				P141
				T142

[illegible]

## 4 Experimental information

Property	Value	Source
Reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	5555	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	EACH PARTICLE	Depositor
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.7	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	169644	Depositor
Image detector	TVIPS TEMCAM-F816 (8k x 8k)	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.97	18/2984 (0.6%)	0.72	15/4040 (0.4%)
1	D	0.93	17/2984 (0.6%)	0.68	13/4040 (0.3%)
1	E	0.93	17/2984 (0.6%)	0.71	15/4040 (0.4%)
1	F	0.93	17/2984 (0.6%)	0.71	15/4040 (0.4%)
1	I	0.93	17/2984 (0.6%)	0.71	15/4040 (0.4%)
2	B	0.36	0/1107	0.31	0/1471
2	H	0.21	0/1107	0.33	0/1471
3	C	0.26	0/5594	0.39	0/7539
3	G	0.22	0/5594	0.38	0/7539
3	J	0.22	0/5594	0.38	0/7539
All	All	0.65	86/33916 (0.3%)	0.55	73/45759 (0.2%)

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
1	A	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	I	0	1
All	All	0	5

All (86) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	166	TYR	CD2-CE2	19.09	1.68	1.39
1	E	166	TYR	CD2-CE2	19.08	1.68	1.39
1	A	166	TYR	CD2-CE2	19.07	1.68	1.39

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	166	TYR	CD2-CE2	19.05	1.68	1.39
1	D	166	TYR	CD2-CE2	19.03	1.67	1.39
1	I	166	TYR	CE2-CZ	18.53	1.62	1.38
1	A	166	TYR	CE2-CZ	18.53	1.62	1.38
1	D	166	TYR	CE2-CZ	18.51	1.62	1.38
1	E	166	TYR	CE2-CZ	18.49	1.62	1.38
1	F	166	TYR	CE2-CZ	18.46	1.62	1.38
1	D	166	TYR	CD1-CE1	18.35	1.66	1.39
1	I	166	TYR	CD1-CE1	18.34	1.66	1.39
1	E	166	TYR	CD1-CE1	18.34	1.66	1.39
1	F	166	TYR	CD1-CE1	18.32	1.66	1.39
1	A	166	TYR	CD1-CE1	18.30	1.66	1.39
1	D	166	TYR	CE1-CZ	15.56	1.58	1.38
1	I	166	TYR	CE1-CZ	15.55	1.58	1.38
1	F	166	TYR	CE1-CZ	15.55	1.58	1.38
1	A	166	TYR	CE1-CZ	15.53	1.58	1.38
1	E	166	TYR	CE1-CZ	15.47	1.58	1.38
1	F	166	TYR	CG-CD1	11.75	1.54	1.39
1	A	166	TYR	CG-CD1	11.74	1.54	1.39
1	I	166	TYR	CG-CD1	11.72	1.54	1.39
1	D	166	TYR	CG-CD1	11.69	1.54	1.39
1	E	166	TYR	CG-CD1	11.69	1.54	1.39
1	D	166	TYR	CG-CD2	11.46	1.54	1.39
1	E	166	TYR	CG-CD2	11.44	1.54	1.39
1	I	166	TYR	CG-CD2	11.43	1.54	1.39
1	F	166	TYR	CG-CD2	11.42	1.53	1.39
1	A	166	TYR	CG-CD2	11.41	1.53	1.39
1	F	150	GLY	N-CA	9.85	1.60	1.46
1	D	150	GLY	N-CA	9.85	1.60	1.46
1	E	150	GLY	N-CA	9.85	1.60	1.46
1	I	150	GLY	N-CA	9.85	1.60	1.46
1	A	150	GLY	N-CA	9.83	1.60	1.46
1	A	333	PRO	N-CD	9.12	1.60	1.47
1	D	41	GLN	N-CA	8.49	1.63	1.46
1	F	41	GLN	N-CA	8.48	1.63	1.46
1	A	41	GLN	N-CA	8.48	1.63	1.46
1	I	41	GLN	N-CA	8.48	1.63	1.46
1	E	41	GLN	N-CA	8.46	1.63	1.46
1	E	149	THR	C-N	6.76	1.45	1.33
1	A	149	THR	C-N	6.75	1.45	1.33
1	D	149	THR	C-N	6.75	1.45	1.33
1	F	149	THR	C-N	6.72	1.45	1.33

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	149	THR	C-N	6.72	1.45	1.33
1	I	47	MET	C-N	6.36	1.44	1.33
1	A	47	MET	C-N	6.35	1.44	1.33
1	D	47	MET	C-N	6.34	1.44	1.33
1	E	47	MET	C-N	6.34	1.44	1.33
1	F	47	MET	C-N	6.32	1.44	1.33
1	F	40	HIS	CB-CG	6.08	1.60	1.50
1	D	40	HIS	CB-CG	6.05	1.60	1.50
1	I	40	HIS	CB-CG	6.05	1.60	1.50
1	A	40	HIS	CB-CG	6.04	1.60	1.50
1	I	43	VAL	CB-CG2	-6.03	1.40	1.52
1	D	43	VAL	CB-CG2	-6.01	1.40	1.52
1	E	40	HIS	CB-CG	6.01	1.60	1.50
1	E	43	VAL	CB-CG2	-6.00	1.40	1.52
1	F	43	VAL	CB-CG2	-5.99	1.40	1.52
1	A	43	VAL	CB-CG2	-5.99	1.40	1.52
1	F	40	HIS	CA-CB	5.53	1.66	1.53
1	E	40	HIS	CA-CB	5.53	1.66	1.53
1	I	40	HIS	CA-CB	5.53	1.66	1.53
1	A	40	HIS	CA-CB	5.52	1.66	1.53
1	D	40	HIS	CA-CB	5.52	1.66	1.53
1	F	48	GLY	N-CA	5.20	1.53	1.46
1	E	48	GLY	N-CA	5.18	1.53	1.46
1	A	48	GLY	N-CA	5.16	1.53	1.46
1	D	43	VAL	CA-CB	5.15	1.65	1.54
1	D	46	GLY	N-CA	5.13	1.53	1.46
1	E	46	GLY	N-CA	5.13	1.53	1.46
1	I	43	VAL	CA-CB	5.13	1.65	1.54
1	I	48	GLY	N-CA	5.12	1.53	1.46
1	F	43	VAL	CA-CB	5.12	1.65	1.54
1	D	48	GLY	N-CA	5.11	1.53	1.46
1	F	46	GLY	N-CA	5.11	1.53	1.46
1	A	43	VAL	CA-CB	5.11	1.65	1.54
1	E	43	VAL	CA-CB	5.11	1.65	1.54
1	A	46	GLY	N-CA	5.09	1.53	1.46
1	I	46	GLY	N-CA	5.09	1.53	1.46
1	D	40	HIS	C-N	5.04	1.45	1.34
1	E	40	HIS	C-N	5.04	1.45	1.34
1	F	40	HIS	C-N	5.04	1.45	1.34
1	A	40	HIS	C-N	5.03	1.45	1.34
1	I	40	HIS	C-N	5.02	1.45	1.34

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	39	ARG	NE-CZ-NH2	-9.45	115.58	120.30
1	E	149	THR	C-N-CA	9.42	142.07	122.30
1	E	39	ARG	NE-CZ-NH2	-9.41	115.59	120.30
1	F	39	ARG	NE-CZ-NH2	-9.40	115.60	120.30
1	I	149	THR	C-N-CA	9.40	142.04	122.30
1	A	149	THR	C-N-CA	9.40	142.04	122.30
1	F	149	THR	C-N-CA	9.39	142.03	122.30
1	D	149	THR	C-N-CA	9.39	142.02	122.30
1	I	39	ARG	NE-CZ-NH2	-9.37	115.62	120.30
1	D	39	ARG	NE-CZ-NH2	-9.36	115.62	120.30
1	E	43	VAL	CA-CB-CG1	9.20	124.70	110.90
1	A	43	VAL	CA-CB-CG1	9.18	124.67	110.90
1	F	43	VAL	CA-CB-CG1	9.18	124.67	110.90
1	D	43	VAL	CA-CB-CG1	9.17	124.65	110.90
1	I	43	VAL	CA-CB-CG1	9.16	124.64	110.90
1	A	53	TYR	CB-CA-C	9.13	128.66	110.40
1	F	53	TYR	CB-CA-C	9.13	128.66	110.40
1	I	53	TYR	CB-CA-C	9.13	128.66	110.40
1	D	53	TYR	CB-CA-C	9.12	128.64	110.40
1	E	53	TYR	CB-CA-C	9.12	128.63	110.40
1	E	47	MET	CA-CB-CG	7.75	126.47	113.30
1	A	47	MET	CA-CB-CG	7.74	126.46	113.30
1	F	47	MET	CA-CB-CG	7.74	126.46	113.30
1	I	47	MET	CA-CB-CG	7.74	126.45	113.30
1	F	47	MET	CB-CA-C	7.26	124.92	110.40
1	E	47	MET	CB-CA-C	7.25	124.90	110.40
1	I	47	MET	CB-CA-C	7.25	124.90	110.40
1	A	47	MET	CB-CA-C	7.24	124.88	110.40
1	D	39	ARG	NE-CZ-NH1	7.24	123.92	120.30
1	A	39	ARG	NE-CZ-NH1	7.20	123.90	120.30
1	E	39	ARG	NE-CZ-NH1	7.18	123.89	120.30
1	I	39	ARG	NE-CZ-NH1	7.12	123.86	120.30
1	F	39	ARG	NE-CZ-NH1	7.10	123.85	120.30
1	D	43	VAL	CG1-CB-CG2	-6.64	100.27	110.90
1	A	43	VAL	CG1-CB-CG2	-6.64	100.27	110.90
1	D	40	HIS	CB-CA-C	6.64	123.68	110.40
1	E	43	VAL	CG1-CB-CG2	-6.64	100.28	110.90
1	E	40	HIS	CB-CA-C	6.63	123.65	110.40
1	F	43	VAL	CG1-CB-CG2	-6.62	100.30	110.90
1	F	40	HIS	CB-CA-C	6.62	123.65	110.40
1	I	43	VAL	CG1-CB-CG2	-6.62	100.31	110.90
1	I	40	HIS	CB-CA-C	6.61	123.63	110.40
1	A	40	HIS	CB-CA-C	6.61	123.62	110.40

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	40	HIS	CA-CB-CG	6.47	124.59	113.60
1	A	40	HIS	CA-CB-CG	6.47	124.59	113.60
1	E	40	HIS	CA-CB-CG	6.46	124.59	113.60
1	I	40	HIS	CA-CB-CG	6.46	124.58	113.60
1	D	40	HIS	CA-CB-CG	6.42	124.52	113.60
1	E	53	TYR	N-CA-CB	6.28	121.90	110.60
1	F	53	TYR	N-CA-CB	6.27	121.88	110.60
1	I	53	TYR	N-CA-CB	6.26	121.87	110.60
1	D	53	TYR	N-CA-CB	6.26	121.87	110.60
1	A	53	TYR	N-CA-CB	6.25	121.86	110.60
1	D	41	GLN	CB-CA-C	-6.09	98.22	110.40
1	I	41	GLN	CB-CA-C	-6.09	98.22	110.40
1	E	41	GLN	CB-CA-C	-6.09	98.23	110.40
1	A	41	GLN	CB-CA-C	-6.08	98.25	110.40
1	F	41	GLN	CB-CA-C	-6.08	98.25	110.40
1	F	41	GLN	N-CA-CB	5.58	120.64	110.60
1	A	41	GLN	N-CA-CB	5.56	120.61	110.60
1	I	41	GLN	N-CA-CB	5.55	120.59	110.60
1	D	41	GLN	N-CA-CB	5.54	120.58	110.60
1	E	41	GLN	N-CA-CB	5.54	120.58	110.60
1	D	52	SER	C-N-CA	5.35	135.07	121.70
1	I	52	SER	C-N-CA	5.34	135.04	121.70
1	A	52	SER	C-N-CA	5.33	135.04	121.70
1	E	52	SER	C-N-CA	5.33	135.03	121.70
1	F	52	SER	C-N-CA	5.31	134.99	121.70
1	F	43	VAL	N-CA-CB	5.21	122.97	111.50
1	D	43	VAL	N-CA-CB	5.21	122.96	111.50
1	A	43	VAL	N-CA-CB	5.21	122.95	111.50
1	E	43	VAL	N-CA-CB	5.20	122.94	111.50
1	I	43	VAL	N-CA-CB	5.20	122.94	111.50

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	40	HIS	Sidechain
1	D	40	HIS	Sidechain
1	E	40	HIS	Sidechain
1	F	40	HIS	Sidechain
1	I	40	HIS	Sidechain

## 5.2 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 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	2934	0	2895	150	0
1	D	2934	0	2895	131	0
1	E	2934	0	2895	125	0
1	F	2934	0	2895	123	0
1	I	2934	0	2895	127	0
2	B	1104	0	1104	3	0
2	H	1104	0	1104	18	0
3	C	5494	0	5492	79	0
3	G	5494	0	5492	89	0
3	J	5494	0	5492	97	0
4	A	27	0	12	4	0
4	D	27	0	12	4	0
4	E	27	0	12	4	0
4	F	27	0	12	4	0
4	I	27	0	12	4	0
5	A	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	I	1	0	0	0	0
All	All	33500	0	33219	834	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 12.

All (834) 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)
1:D:54:VAL:HG22	1:D:55:GLY:H	1.10	1.14
1:A:54:VAL:HG22	1:A:55:GLY:H	1.10	1.10
1:I:54:VAL:HG22	1:I:55:GLY:H	1.10	1.10
1:F:54:VAL:HG22	1:F:55:GLY:H	1.10	1.08
1:E:54:VAL:HG22	1:E:55:GLY:H	1.10	1.07
1:E:54:VAL:HG22	1:E:55:GLY:N	1.73	1.03
1:F:54:VAL:HG22	1:F:55:GLY:N	1.73	1.02

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:54:VAL:HG22	1:I:55:GLY:N	1.73	1.02
1:A:54:VAL:HG22	1:A:55:GLY:N	1.73	1.01
1:E:40:HIS:CD2	1:F:167:GLU:HB3	1.95	1.01
1:D:54:VAL:HG22	1:D:55:GLY:N	1.73	1.01
1:A:55:GLY:HA3	1:A:88:HIS:CE1	1.96	1.00
1:F:55:GLY:HA3	1:F:88:HIS:CE1	1.96	1.00
1:I:55:GLY:HA3	1:I:88:HIS:CE1	1.96	1.00
1:E:55:GLY:HA3	1:E:88:HIS:CE1	1.96	0.99
1:D:55:GLY:HA3	1:D:88:HIS:CE1	1.96	0.99
2:H:226:LYS:HG3	3:J:285:ALA:HB3	1.45	0.98
1:A:40:HIS:CD2	1:I:167:GLU:HB3	1.99	0.98
1:A:167:GLU:HB3	1:D:40:HIS:CD2	1.98	0.98
1:A:54:VAL:CG2	1:A:55:GLY:H	1.78	0.97
1:I:54:VAL:CG2	1:I:55:GLY:H	1.78	0.97
1:D:54:VAL:CG2	1:D:55:GLY:H	1.78	0.96
1:F:54:VAL:CG2	1:F:55:GLY:H	1.78	0.96
1:E:54:VAL:CG2	1:E:55:GLY:H	1.78	0.95
1:A:170:ALA:HB3	1:D:41:GLN:NE2	1.84	0.93
1:D:43:VAL:HG23	1:D:46:GLY:H	1.33	0.93
1:A:41:GLN:NE2	1:I:170:ALA:HB3	1.83	0.93
1:A:43:VAL:HG23	1:A:46:GLY:H	1.33	0.92
3:G:107:LYS:HD3	3:G:107:LYS:N	1.85	0.91
1:I:43:VAL:HG23	1:I:46:GLY:H	1.33	0.91
1:F:43:VAL:HG23	1:F:46:GLY:H	1.33	0.90
3:J:107:LYS:N	3:J:107:LYS:HD3	1.86	0.90
1:D:51:ASP:O	1:D:53:TYR:N	2.05	0.90
1:A:51:ASP:O	1:A:53:TYR:N	2.05	0.90
1:E:43:VAL:HG23	1:E:46:GLY:H	1.33	0.90
1:I:51:ASP:O	1:I:53:TYR:N	2.05	0.90
1:F:51:ASP:O	1:F:53:TYR:N	2.05	0.89
3:C:106:GLY:C	3:C:108:THR:H	1.66	0.89
1:E:51:ASP:O	1:E:53:TYR:N	2.05	0.88
1:E:41:GLN:NE2	1:F:170:ALA:HB3	1.87	0.87
3:G:107:LYS:HD3	3:G:107:LYS:H	1.39	0.87
3:J:107:LYS:HD3	3:J:107:LYS:H	1.39	0.86
1:I:38:PRO:HG3	1:I:49:GLN:HG2	1.59	0.85
1:A:42:GLY:C	1:I:167:GLU:O	2.14	0.85
1:A:38:PRO:HG3	1:A:49:GLN:HG2	1.58	0.85
1:D:38:PRO:HG3	1:D:49:GLN:HG2	1.58	0.84
1:F:38:PRO:HG3	1:F:49:GLN:HG2	1.58	0.84
1:I:51:ASP:C	1:I:53:TYR:H	1.81	0.83

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:GLU:O	1:D:42:GLY:C	2.17	0.83
1:A:51:ASP:C	1:A:53:TYR:H	1.81	0.83
1:E:38:PRO:HG3	1:E:49:GLN:HG2	1.58	0.83
1:D:51:ASP:C	1:D:53:TYR:H	1.81	0.82
1:E:41:GLN:HE22	1:F:169:TYR:C	1.81	0.82
1:F:157:ASP:HB3	4:F:376:ADP:O3B	1.80	0.82
1:E:171:LEU:HB2	1:E:172:PRO:HD2	1.63	0.81
1:F:171:LEU:HB2	1:F:172:PRO:HD2	1.63	0.81
1:I:157:ASP:HB3	4:I:376:ADP:O3B	1.80	0.81
1:A:157:ASP:HB3	4:A:376:ADP:O3B	1.80	0.81
1:I:38:PRO:HG3	1:I:49:GLN:CG	2.11	0.81
3:C:106:GLY:C	3:C:108:THR:N	2.32	0.81
1:D:157:ASP:HB3	4:D:376:ADP:O3B	1.80	0.81
1:A:38:PRO:HG3	1:A:49:GLN:CG	2.11	0.81
1:E:157:ASP:HB3	4:E:376:ADP:O3B	1.80	0.80
1:D:171:LEU:HB2	1:D:172:PRO:HD2	1.63	0.80
2:H:222:GLU:OE1	3:J:286:GLU:HG3	1.82	0.80
1:A:40:HIS:HD2	1:I:167:GLU:HB3	1.46	0.80
1:D:38:PRO:HG3	1:D:49:GLN:CG	2.11	0.80
1:F:38:PRO:HG3	1:F:49:GLN:CG	2.11	0.80
1:E:42:GLY:C	1:F:167:GLU:O	2.19	0.80
1:A:171:LEU:HB2	1:A:172:PRO:HD2	1.63	0.80
1:E:38:PRO:HG3	1:E:49:GLN:CG	2.11	0.80
1:I:171:LEU:HB2	1:I:172:PRO:HD2	1.63	0.79
1:A:167:GLU:HB3	1:D:40:HIS:HD2	1.45	0.79
1:F:55:GLY:CA	1:F:88:HIS:CE1	2.66	0.78
1:E:34:ILE:O	1:E:35:VAL:HG23	1.83	0.78
1:E:51:ASP:C	1:E:53:TYR:H	1.81	0.78
1:I:34:ILE:O	1:I:35:VAL:HG23	1.83	0.78
1:A:168:GLY:O	1:D:40:HIS:CE1	2.37	0.78
1:F:51:ASP:C	1:F:53:TYR:H	1.81	0.78
1:A:34:ILE:O	1:A:35:VAL:HG23	1.83	0.77
1:E:40:HIS:HD2	1:F:167:GLU:HB3	1.44	0.77
1:F:34:ILE:O	1:F:35:VAL:HG23	1.83	0.77
1:I:55:GLY:CA	1:I:88:HIS:CE1	2.66	0.77
3:C:560:GLU:O	3:C:560:GLU:HG3	1.83	0.77
1:D:55:GLY:CA	1:D:88:HIS:CE1	2.66	0.77
1:E:55:GLY:CA	1:E:88:HIS:CE1	2.66	0.77
1:E:40:HIS:CE1	1:F:168:GLY:H	2.03	0.77
1:A:55:GLY:CA	1:A:88:HIS:CE1	2.66	0.77
3:G:286:GLU:HG3	2:H:145:GLU:OE1	1.84	0.77

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:34:ILE:O	1:D:35:VAL:HG23	1.83	0.76
3:J:58:LYS:O	3:J:60:SER:N	2.19	0.76
3:G:58:LYS:O	3:G:60:SER:N	2.19	0.76
1:D:83:GLU:HG2	1:D:87:HIS:CE1	2.21	0.76
1:A:40:HIS:CE1	1:I:168:GLY:O	2.39	0.75
3:C:58:LYS:O	3:C:60:SER:N	2.19	0.75
1:E:53:TYR:HB3	1:E:57:GLU:OE1	1.87	0.74
1:A:43:VAL:N	1:I:168:GLY:HA2	2.02	0.74
1:I:53:TYR:HB3	1:I:57:GLU:OE1	1.87	0.74
1:A:55:GLY:O	1:A:57:GLU:N	2.21	0.74
1:F:55:GLY:C	1:F:57:GLU:H	1.90	0.74
1:E:55:GLY:C	1:E:57:GLU:H	1.90	0.74
1:E:40:HIS:CE1	1:F:168:GLY:O	2.39	0.74
1:F:53:TYR:HB3	1:F:57:GLU:OE1	1.87	0.74
1:A:53:TYR:HB3	1:A:57:GLU:OE1	1.87	0.74
1:F:55:GLY:O	1:F:57:GLU:N	2.21	0.74
3:G:328:GLY:O	3:G:330:GLY:N	2.20	0.74
3:C:328:GLY:O	3:C:330:GLY:N	2.21	0.74
1:D:53:TYR:HB3	1:D:57:GLU:OE1	1.87	0.74
1:D:55:GLY:C	1:D:57:GLU:H	1.90	0.74
1:D:55:GLY:O	1:D:57:GLU:N	2.21	0.74
1:A:55:GLY:C	1:A:57:GLU:H	1.90	0.74
1:E:55:GLY:O	1:E:57:GLU:N	2.21	0.74
3:J:328:GLY:O	3:J:330:GLY:N	2.21	0.73
1:I:55:GLY:O	1:I:57:GLU:N	2.21	0.73
1:A:168:GLY:H	1:D:40:HIS:CE1	2.05	0.73
1:I:55:GLY:C	1:I:57:GLU:H	1.90	0.73
1:A:168:GLY:O	1:D:40:HIS:HE1	1.72	0.72
1:A:37:ARG:HG3	1:A:38:PRO:HD3	1.71	0.72
1:E:37:ARG:HG3	1:E:38:PRO:HD3	1.71	0.72
1:I:37:ARG:HG3	1:I:38:PRO:HD3	1.72	0.72
1:F:37:ARG:HG3	1:F:38:PRO:HD3	1.71	0.72
1:F:43:VAL:HG23	1:F:46:GLY:N	2.05	0.72
3:C:482:GLU:OE2	3:C:489:SER:OG	2.06	0.72
3:G:323:ARG:O	3:G:337:SER:OG	2.06	0.72
1:I:36:GLY:O	1:I:52:SER:HA	1.90	0.72
1:A:36:GLY:O	1:A:52:SER:HA	1.90	0.72
1:D:37:ARG:HG3	1:D:38:PRO:HD3	1.72	0.72
1:E:40:HIS:HE1	1:F:168:GLY:O	1.72	0.72
1:D:36:GLY:O	1:D:52:SER:HA	1.90	0.71
3:J:323:ARG:O	3:J:337:SER:OG	2.06	0.71

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:VAL:N	1:I:167:GLU:O	2.22	0.71
1:A:168:GLY:HA2	1:D:43:VAL:N	2.05	0.71
2:H:222:GLU:OE1	3:J:286:GLU:HA	1.91	0.71
1:E:36:GLY:O	1:E:52:SER:HA	1.90	0.71
1:E:36:GLY:O	1:E:52:SER:CA	2.39	0.71
1:E:49:GLN:HG3	1:E:50:LYS:N	2.06	0.71
1:F:36:GLY:O	1:F:52:SER:CA	2.39	0.71
1:F:36:GLY:O	1:F:52:SER:HA	1.90	0.70
1:D:43:VAL:HG23	1:D:46:GLY:N	2.05	0.70
1:A:40:HIS:CE1	1:I:168:GLY:H	2.07	0.70
1:A:43:VAL:HG23	1:A:46:GLY:N	2.05	0.70
1:I:36:GLY:O	1:I:52:SER:CA	2.39	0.70
1:I:49:GLN:HG3	1:I:50:LYS:N	2.06	0.70
1:A:36:GLY:O	1:A:52:SER:CA	2.39	0.70
3:J:482:GLU:OE2	3:J:489:SER:OG	2.06	0.70
1:F:42:GLY:C	1:F:44:MET:H	1.94	0.70
1:E:43:VAL:N	1:F:167:GLU:O	2.24	0.70
1:F:49:GLN:HG3	1:F:50:LYS:N	2.06	0.70
1:D:36:GLY:O	1:D:52:SER:CA	2.39	0.70
1:I:43:VAL:HG23	1:I:46:GLY:N	2.05	0.70
1:A:167:GLU:O	1:D:43:VAL:N	2.25	0.69
1:E:42:GLY:C	1:E:44:MET:H	1.94	0.69
1:A:49:GLN:HG3	1:A:50:LYS:N	2.06	0.69
1:D:49:GLN:HG3	1:D:50:LYS:N	2.06	0.69
1:A:43:VAL:H	1:I:168:GLY:HA2	1.58	0.69
1:A:40:HIS:HE1	1:I:168:GLY:O	1.75	0.68
1:E:43:VAL:HG23	1:E:46:GLY:N	2.05	0.68
1:D:42:GLY:C	1:D:44:MET:H	1.94	0.67
1:D:37:ARG:HH11	1:D:37:ARG:HG3	1.59	0.67
3:G:19:ILE:HG23	3:G:19:ILE:O	1.95	0.67
1:A:37:ARG:HG3	1:A:37:ARG:HH11	1.59	0.67
1:I:42:GLY:C	1:I:44:MET:H	1.94	0.67
1:F:54:VAL:CG2	1:F:55:GLY:N	2.43	0.67
1:I:37:ARG:HH11	1:I:37:ARG:HG3	1.60	0.67
1:E:37:ARG:CG	1:E:37:ARG:HH11	2.08	0.67
1:F:37:ARG:HH11	1:F:37:ARG:CG	2.08	0.67
3:G:287:GLN:O	2:H:149:LYS:HE2	1.95	0.67
1:A:42:GLY:C	1:A:44:MET:H	1.94	0.67
3:C:19:ILE:O	3:C:19:ILE:HG23	1.95	0.66
3:J:19:ILE:O	3:J:19:ILE:HG23	1.95	0.66
3:J:80:LEU:O	3:J:84:ALA:N	2.29	0.66

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:54:VAL:CG2	1:E:55:GLY:N	2.43	0.66
3:C:80:LEU:O	3:C:84:ALA:N	2.29	0.66
1:D:37:ARG:HH11	1:D:37:ARG:CG	2.08	0.66
1:E:43:VAL:N	1:F:168:GLY:HA2	2.09	0.66
1:A:37:ARG:CG	1:A:37:ARG:HH11	2.08	0.66
1:I:37:ARG:CG	1:I:37:ARG:HH11	2.08	0.66
1:A:168:GLY:HA2	1:D:43:VAL:H	1.61	0.65
3:G:482:GLU:OE2	3:G:489:SER:OG	2.06	0.65
3:J:622:ALA:HB3	3:J:678:PHE:CE2	2.31	0.65
3:C:106:GLY:O	3:C:108:THR:N	2.30	0.65
1:E:37:ARG:HG3	1:E:37:ARG:HH11	1.59	0.65
3:G:80:LEU:O	3:G:84:ALA:N	2.29	0.65
2:H:226:LYS:HG3	3:J:285:ALA:CB	2.22	0.65
3:C:622:ALA:HB3	3:C:678:PHE:CE2	2.31	0.65
1:D:53:TYR:C	1:D:58:ALA:HB2	2.18	0.64
1:E:36:GLY:O	1:E:52:SER:HB3	1.98	0.64
1:F:37:ARG:HH11	1:F:37:ARG:HG3	1.59	0.64
1:I:36:GLY:O	1:I:52:SER:HB3	1.98	0.64
1:E:53:TYR:C	1:E:58:ALA:HB2	2.18	0.64
1:A:53:TYR:C	1:A:58:ALA:HB2	2.18	0.64
3:J:625:ALA:O	3:J:627:ARG:NH1	2.30	0.64
1:F:36:GLY:O	1:F:52:SER:HB3	1.98	0.64
3:G:622:ALA:HB3	3:G:678:PHE:CE2	2.31	0.64
1:A:36:GLY:O	1:A:52:SER:HB3	1.98	0.64
3:G:625:ALA:O	3:G:627:ARG:NH1	2.30	0.64
1:I:54:VAL:CG2	1:I:55:GLY:N	2.43	0.64
3:C:625:ALA:O	3:C:627:ARG:NH1	2.30	0.64
1:D:36:GLY:O	1:D:52:SER:HB3	1.98	0.64
1:F:53:TYR:C	1:F:58:ALA:HB2	2.18	0.64
1:A:39:ARG:HB3	1:A:66:THR:OG1	1.98	0.64
1:E:39:ARG:HB3	1:E:66:THR:OG1	1.98	0.64
1:I:53:TYR:C	1:I:58:ALA:HB2	2.18	0.64
1:D:349:LEU:HD22	3:J:461:GLU:HA	1.80	0.63
1:F:39:ARG:HB3	1:F:66:THR:OG1	1.98	0.63
1:I:39:ARG:HB3	1:I:66:THR:OG1	1.98	0.62
1:A:54:VAL:CG2	1:A:55:GLY:N	2.43	0.62
1:D:39:ARG:HB3	1:D:66:THR:OG1	1.98	0.62
1:A:43:VAL:HA	1:I:168:GLY:HA2	1.82	0.62
2:H:226:LYS:CG	3:J:285:ALA:HB3	2.26	0.62
1:D:150:GLY:O	1:D:166:TYR:CG	2.53	0.62
1:E:107:GLU:HB2	1:E:134:VAL:HG22	1.82	0.62

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:GLY:O	1:A:166:TYR:CG	2.53	0.62
1:E:150:GLY:O	1:E:166:TYR:CG	2.53	0.61
1:E:43:VAL:H	1:F:168:GLY:HA2	1.65	0.61
3:C:334:GLU:O	3:C:335:VAL:HB	2.00	0.61
1:F:26:ALA:O	1:F:28:ARG:NH1	2.34	0.61
3:G:529:GLY:O	3:G:532:ILE:N	2.34	0.61
1:D:54:VAL:CG2	1:D:55:GLY:N	2.43	0.61
1:E:43:VAL:HA	1:F:168:GLY:HA2	1.83	0.61
1:I:150:GLY:O	1:I:166:TYR:CG	2.53	0.61
1:A:45:VAL:C	1:A:47:MET:H	2.04	0.61
1:D:107:GLU:HB2	1:D:134:VAL:HG22	1.82	0.61
1:A:107:GLU:HB2	1:A:134:VAL:HG22	1.82	0.61
3:C:529:GLY:O	3:C:532:ILE:N	2.34	0.61
1:F:107:GLU:HB2	1:F:134:VAL:HG22	1.82	0.61
1:F:150:GLY:O	1:F:166:TYR:CG	2.53	0.61
1:F:45:VAL:C	1:F:47:MET:H	2.04	0.61
1:I:26:ALA:O	1:I:28:ARG:NH1	2.33	0.61
3:J:136:LEU:O	3:J:139:SER:OG	2.19	0.61
1:I:107:GLU:HB2	1:I:134:VAL:HG22	1.82	0.61
3:J:529:GLY:O	3:J:532:ILE:N	2.34	0.60
1:A:43:VAL:CA	1:I:168:GLY:HA2	2.31	0.60
1:E:45:VAL:C	1:E:47:MET:H	2.04	0.60
1:D:26:ALA:O	1:D:28:ARG:NH1	2.33	0.60
1:E:26:ALA:O	1:E:28:ARG:NH1	2.33	0.60
1:A:168:GLY:HA2	1:D:43:VAL:HA	1.83	0.60
1:E:171:LEU:HB2	1:E:172:PRO:CD	2.31	0.60
1:D:45:VAL:C	1:D:47:MET:H	2.04	0.60
1:I:45:VAL:C	1:I:47:MET:H	2.04	0.60
3:C:365:VAL:O	3:C:369:ASN:ND2	2.35	0.59
1:A:171:LEU:HB2	1:A:172:PRO:CD	2.31	0.59
3:G:91:SER:O	3:G:92:GLN:HB3	2.02	0.59
1:I:171:LEU:HB2	1:I:172:PRO:CD	2.31	0.59
3:J:645:TRP:O	3:J:647:SER:N	2.35	0.59
3:J:365:VAL:O	3:J:369:ASN:ND2	2.35	0.59
3:C:645:TRP:O	3:C:647:SER:N	2.35	0.59
1:F:171:LEU:HB2	1:F:172:PRO:CD	2.31	0.59
3:G:645:TRP:O	3:G:647:SER:N	2.35	0.59
1:F:55:GLY:HA3	1:F:88:HIS:NE2	2.17	0.59
3:G:365:VAL:O	3:G:369:ASN:ND2	2.35	0.59
3:J:91:SER:O	3:J:92:GLN:HB3	2.03	0.59
3:C:91:SER:O	3:C:92:GLN:HB3	2.02	0.59

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:515:ASP:OD1	3:G:516:VAL:N	2.36	0.58
1:E:55:GLY:HA3	1:E:88:HIS:NE2	2.17	0.58
1:I:38:PRO:CG	1:I:49:GLN:HG2	2.33	0.58
3:J:515:ASP:OD1	3:J:516:VAL:N	2.36	0.58
3:C:136:LEU:O	3:C:139:SER:OG	2.19	0.58
1:A:43:VAL:CG2	1:A:46:GLY:HA3	2.34	0.58
3:J:336:ILE:O	3:J:337:SER:OG	2.22	0.58
3:C:515:ASP:OD1	3:C:516:VAL:N	2.36	0.58
1:I:43:VAL:CG2	1:I:46:GLY:HA3	2.34	0.58
2:H:226:LYS:CG	3:J:285:ALA:CB	2.82	0.58
1:D:43:VAL:CG2	1:D:46:GLY:HA3	2.34	0.58
1:F:42:GLY:O	1:F:43:VAL:HG22	2.04	0.58
1:E:38:PRO:CG	1:E:49:GLN:HG2	2.33	0.57
3:G:336:ILE:O	3:G:337:SER:OG	2.22	0.57
1:E:40:HIS:NE2	1:F:168:GLY:N	2.50	0.57
3:J:645:TRP:HB3	3:J:646:PRO:HD2	1.86	0.57
1:A:168:GLY:HA2	1:D:43:VAL:CA	2.34	0.57
1:I:42:GLY:O	1:I:43:VAL:HG22	2.04	0.57
1:A:42:GLY:O	1:A:43:VAL:HG22	2.04	0.57
1:A:55:GLY:C	1:A:57:GLU:N	2.58	0.57
1:D:55:GLY:C	1:D:57:GLU:N	2.58	0.57
1:E:42:GLY:O	1:E:43:VAL:HG22	2.04	0.57
1:D:42:GLY:O	1:D:43:VAL:HG22	2.04	0.57
1:D:55:GLY:HA3	1:D:88:HIS:NE2	2.18	0.57
1:E:55:GLY:C	1:E:57:GLU:N	2.58	0.57
1:F:43:VAL:CG2	1:F:46:GLY:HA3	2.34	0.57
1:A:55:GLY:HA3	1:A:88:HIS:NE2	2.17	0.57
3:C:645:TRP:HB3	3:C:646:PRO:HD2	1.86	0.57
1:I:143:TYR:HH	1:I:169:TYR:HH	1.53	0.57
3:J:234:CYS:SG	3:J:235:PHE:N	2.78	0.56
3:C:234:CYS:SG	3:C:235:PHE:N	2.78	0.56
1:E:43:VAL:CG2	1:E:46:GLY:HA3	2.34	0.56
1:F:38:PRO:CG	1:F:49:GLN:HG2	2.33	0.56
3:G:645:TRP:HB3	3:G:646:PRO:HD2	1.86	0.56
1:D:171:LEU:HB2	1:D:172:PRO:CD	2.31	0.56
1:E:43:VAL:CA	1:F:168:GLY:HA2	2.35	0.56
1:F:55:GLY:C	1:F:57:GLU:N	2.58	0.56
2:H:222:GLU:CD	3:J:286:GLU:HA	2.26	0.56
1:I:37:ARG:NH1	1:I:37:ARG:CG	2.68	0.56
1:A:38:PRO:CG	1:A:49:GLN:HG2	2.33	0.56
3:G:234:CYS:SG	3:G:235:PHE:N	2.78	0.56

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:55:GLY:HA3	1:I:88:HIS:NE2	2.17	0.56
1:I:288:ASP:OD1	1:I:291:LYS:NZ	2.39	0.56
1:A:288:ASP:OD1	1:A:291:LYS:NZ	2.39	0.56
1:F:288:ASP:OD1	1:F:291:LYS:NZ	2.39	0.55
3:G:462:ALA:O	3:G:468:SER:OG	2.24	0.55
1:A:37:ARG:CG	1:A:37:ARG:NH1	2.68	0.55
1:E:288:ASP:OD1	1:E:291:LYS:NZ	2.39	0.55
1:E:40:HIS:CE1	1:F:168:GLY:N	2.74	0.55
3:G:461:GLU:HA	1:I:349:LEU:HD22	1.88	0.55
1:A:349:LEU:HD22	3:C:461:GLU:HA	1.88	0.55
1:A:42:GLY:O	1:I:167:GLU:O	2.23	0.55
3:G:136:LEU:O	3:G:139:SER:OG	2.19	0.55
3:J:462:ALA:O	3:J:468:SER:OG	2.24	0.55
3:G:550:THR:HG22	3:G:551:ARG:HG3	1.88	0.55
3:J:550:THR:HG22	3:J:551:ARG:HG3	1.88	0.55
1:E:252:ASN:OD1	1:E:256:ARG:NH2	2.40	0.55
1:I:270:GLU:N	1:I:270:GLU:OE1	2.40	0.55
1:D:270:GLU:OE1	1:D:270:GLU:N	2.40	0.54
1:F:252:ASN:OD1	1:F:256:ARG:NH2	2.40	0.54
3:J:628:ILE:O	3:J:677:VAL:N	2.39	0.54
1:A:252:ASN:OD1	1:A:256:ARG:NH2	2.40	0.54
1:E:43:VAL:HG13	1:F:167:GLU:O	2.07	0.54
3:C:550:THR:HG22	3:C:551:ARG:HG3	1.88	0.54
1:A:270:GLU:N	1:A:270:GLU:OE1	2.40	0.54
1:D:252:ASN:OD1	1:D:256:ARG:NH2	2.40	0.54
1:A:168:GLY:N	1:D:40:HIS:NE2	2.51	0.54
1:E:270:GLU:OE1	1:E:270:GLU:N	2.40	0.54
1:F:270:GLU:N	1:F:270:GLU:OE1	2.40	0.54
1:I:2:GLU:OE1	1:I:3:ASP:N	2.41	0.54
3:C:494:LYS:HB3	1:D:99:GLU:OE1	2.07	0.54
1:F:2:GLU:OE1	1:F:3:ASP:N	2.41	0.54
1:I:35:VAL:HG13	1:I:52:SER:CB	2.38	0.54
1:D:37:ARG:NH1	1:D:37:ARG:CG	2.68	0.54
1:E:37:ARG:CG	1:E:37:ARG:NH1	2.68	0.54
1:I:252:ASN:OD1	1:I:256:ARG:NH2	2.40	0.54
3:G:628:ILE:O	3:G:677:VAL:N	2.39	0.54
1:A:35:VAL:HG13	1:A:52:SER:CB	2.38	0.53
1:A:41:GLN:CD	1:I:170:ALA:HB3	2.28	0.53
1:E:2:GLU:OE1	1:E:3:ASP:N	2.41	0.53
1:F:87:HIS:O	1:F:87:HIS:ND1	2.41	0.53
3:G:518:GLY:O	3:G:520:LEU:N	2.42	0.53

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:83:GLU:O	1:D:87:HIS:CD2	2.61	0.53
1:E:336:LYS:HE3	4:E:376:ADP:O2A	2.09	0.53
1:I:336:LYS:HE3	4:I:376:ADP:O2A	2.09	0.53
1:D:2:GLU:OE1	1:D:3:ASP:N	2.41	0.53
1:D:36:GLY:O	1:D:52:SER:CB	2.57	0.53
1:A:336:LYS:HE3	4:A:376:ADP:O2A	2.08	0.53
1:A:87:HIS:O	1:A:87:HIS:ND1	2.41	0.53
1:D:143:TYR:OH	1:D:169:TYR:OH	2.27	0.53
1:E:87:HIS:O	1:E:87:HIS:ND1	2.41	0.53
1:F:336:LYS:HE3	4:F:376:ADP:O2A	2.09	0.53
1:I:38:PRO:HG3	1:I:49:GLN:CD	2.29	0.53
2:H:222:GLU:OE2	3:J:286:GLU:CA	2.56	0.53
2:H:222:GLU:OE2	3:J:286:GLU:HA	2.08	0.53
1:A:167:GLU:O	1:D:42:GLY:O	2.26	0.53
1:D:336:LYS:HE3	4:D:376:ADP:O2A	2.09	0.53
1:F:35:VAL:HG13	1:F:52:SER:CB	2.38	0.53
1:I:87:HIS:O	1:I:87:HIS:ND1	2.41	0.53
1:F:107:GLU:N	1:F:135:ALA:O	2.42	0.53
1:A:36:GLY:O	1:A:52:SER:CB	2.57	0.53
3:C:529:GLY:O	3:C:531:LEU:N	2.42	0.53
1:D:38:PRO:HG3	1:D:49:GLN:CD	2.29	0.53
1:A:43:VAL:H	1:I:168:GLY:CA	2.22	0.53
1:D:107:GLU:N	1:D:135:ALA:O	2.42	0.53
1:D:35:VAL:HG13	1:D:52:SER:CB	2.38	0.53
1:E:36:GLY:O	1:E:52:SER:CB	2.57	0.53
1:I:107:GLU:N	1:I:135:ALA:O	2.42	0.53
3:J:518:GLY:O	3:J:520:LEU:N	2.42	0.53
3:C:518:GLY:O	3:C:520:LEU:N	2.42	0.52
1:D:50:LYS:HG2	1:D:51:ASP:N	2.24	0.52
1:F:36:GLY:O	1:F:52:SER:CB	2.57	0.52
3:J:91:SER:O	3:J:92:GLN:CB	2.57	0.52
1:A:43:VAL:HG21	1:A:46:GLY:HA3	1.92	0.52
3:C:621:ARG:HD2	3:C:627:ARG:HD2	1.92	0.52
1:D:38:PRO:CG	1:D:49:GLN:HG2	2.33	0.52
1:I:36:GLY:O	1:I:52:SER:CB	2.57	0.52
1:A:170:ALA:HB3	1:D:41:GLN:HE22	1.69	0.52
1:D:43:VAL:HG21	1:D:46:GLY:HA3	1.92	0.52
1:E:107:GLU:N	1:E:135:ALA:O	2.42	0.52
1:E:202:THR:N	1:E:205:GLU:OE2	2.42	0.52
1:E:35:VAL:HG13	1:E:52:SER:CB	2.38	0.52
3:G:529:GLY:O	3:G:531:LEU:N	2.42	0.52

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:VAL:HG13	1:I:167:GLU:O	2.10	0.52
1:I:202:THR:N	1:I:205:GLU:OE2	2.42	0.52
3:G:621:ARG:HD2	3:G:627:ARG:HD2	1.92	0.52
3:J:529:GLY:O	3:J:531:LEU:N	2.42	0.52
1:A:202:THR:N	1:A:205:GLU:OE2	2.42	0.52
1:I:43:VAL:HG21	1:I:46:GLY:HA3	1.92	0.52
1:A:107:GLU:N	1:A:135:ALA:O	2.42	0.52
1:A:38:PRO:HG3	1:A:49:GLN:CD	2.29	0.52
1:A:167:GLU:O	1:D:43:VAL:HG13	2.09	0.52
1:E:41:GLN:NE2	1:F:169:TYR:C	2.43	0.52
3:C:91:SER:O	3:C:92:GLN:CB	2.57	0.52
1:A:170:ALA:HB3	1:D:41:GLN:CD	2.28	0.52
1:E:37:ARG:CB	1:E:38:PRO:CD	2.88	0.52
1:E:38:PRO:HG3	1:E:49:GLN:CD	2.29	0.52
3:J:621:ARG:HD2	3:J:627:ARG:HD2	1.92	0.52
1:A:168:GLY:N	1:D:40:HIS:CE1	2.76	0.52
1:A:276:GLU:OE1	1:A:276:GLU:N	2.43	0.52
1:A:37:ARG:CB	1:A:38:PRO:CD	2.88	0.52
1:D:37:ARG:CB	1:D:38:PRO:CD	2.88	0.52
1:F:276:GLU:N	1:F:276:GLU:OE1	2.43	0.52
1:E:276:GLU:OE1	1:E:276:GLU:N	2.43	0.52
1:I:276:GLU:OE1	1:I:276:GLU:N	2.43	0.52
3:C:628:ILE:O	3:C:677:VAL:N	2.39	0.52
1:D:276:GLU:N	1:D:276:GLU:OE1	2.43	0.51
1:E:41:GLN:HE22	1:F:170:ALA:HB3	1.70	0.51
1:A:41:GLN:HE22	1:I:170:ALA:HB3	1.69	0.51
1:A:40:HIS:NE2	1:I:168:GLY:N	2.54	0.51
3:J:442:LYS:N	3:J:443:PRO:HD3	2.26	0.51
1:A:280:ASN:OD1	1:A:284:LYS:NZ	2.43	0.51
1:F:38:PRO:HG3	1:F:49:GLN:CD	2.29	0.51
3:G:201:ILE:HG13	3:G:270:LEU:HD11	1.93	0.51
3:G:91:SER:O	3:G:92:GLN:CB	2.57	0.51
1:I:37:ARG:CB	1:I:38:PRO:CD	2.88	0.51
3:C:442:LYS:N	3:C:443:PRO:HD3	2.26	0.51
1:F:280:ASN:OD1	1:F:284:LYS:NZ	2.43	0.51
1:I:173:HIS:CG	1:I:174:ALA:N	2.78	0.51
3:J:201:ILE:HG13	3:J:270:LEU:HD11	1.93	0.51
3:C:201:ILE:HG13	3:C:270:LEU:HD11	1.93	0.51
1:D:349:LEU:HD13	3:J:461:GLU:HG2	1.92	0.51
3:G:442:LYS:N	3:G:443:PRO:HD3	2.26	0.51
1:D:53:TYR:CB	1:D:57:GLU:OE1	2.58	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:43:VAL:HG21	1:F:46:GLY:HA3	1.91	0.51
1:F:66:THR:HG23	1:I:270:GLU:HG3	1.93	0.51
1:E:43:VAL:HG21	1:E:46:GLY:HA3	1.92	0.51
1:F:37:ARG:CB	1:F:38:PRO:CD	2.88	0.51
1:E:173:HIS:CG	1:E:174:ALA:N	2.78	0.51
1:E:34:ILE:O	1:E:35:VAL:CG2	2.57	0.51
1:F:173:HIS:CG	1:F:174:ALA:N	2.78	0.51
1:D:173:HIS:CG	1:D:174:ALA:N	2.78	0.50
3:G:282:ALA:O	3:G:283:GLU:C	2.50	0.50
3:J:463:CYS:HA	3:J:520:LEU:HD22	1.92	0.50
1:D:288:ASP:OD1	1:D:291:LYS:NZ	2.39	0.50
3:G:548:PRO:O	3:G:550:THR:N	2.41	0.50
2:B:221:TYR:OH	3:J:286:GLU:OE2	2.29	0.50
1:E:280:ASN:OD1	1:E:284:LYS:NZ	2.43	0.50
1:I:40:HIS:O	1:I:41:GLN:OE1	2.30	0.50
3:C:41:ILE:HG22	3:C:44:VAL:HB	1.94	0.50
3:C:560:GLU:O	3:C:560:GLU:CG	2.56	0.50
1:E:42:GLY:O	1:F:167:GLU:O	2.29	0.50
1:A:173:HIS:CG	1:A:174:ALA:N	2.78	0.50
1:E:40:HIS:O	1:E:41:GLN:OE1	2.30	0.50
1:F:53:TYR:CB	1:F:57:GLU:OE1	2.58	0.50
1:D:202:THR:N	1:D:205:GLU:OE2	2.42	0.50
1:F:202:THR:N	1:F:205:GLU:OE2	2.42	0.50
3:G:679:ILE:HG21	3:G:684:THR:HG21	1.93	0.50
1:A:40:HIS:O	1:A:41:GLN:OE1	2.30	0.50
3:C:282:ALA:O	3:C:283:GLU:C	2.50	0.50
1:D:54:VAL:O	1:D:55:GLY:O	2.30	0.50
1:A:54:VAL:O	1:A:55:GLY:O	2.30	0.50
1:F:40:HIS:O	1:F:41:GLN:OE1	2.30	0.50
3:G:463:CYS:HA	3:G:520:LEU:HD22	1.92	0.50
3:J:548:PRO:O	3:J:550:THR:N	2.41	0.50
3:J:601:GLU:OE2	3:J:605:ARG:NH2	2.45	0.50
1:A:40:HIS:CE1	1:I:168:GLY:N	2.78	0.50
1:D:40:HIS:O	1:D:41:GLN:OE1	2.30	0.49
1:I:54:VAL:O	1:I:55:GLY:O	2.30	0.49
3:J:282:ALA:O	3:J:283:GLU:C	2.50	0.49
3:C:463:CYS:HA	3:C:520:LEU:HD22	1.93	0.49
1:E:35:VAL:HG12	1:E:35:VAL:O	2.12	0.49
3:J:140:ASN:HB2	3:J:141:PRO:HD3	1.94	0.49
1:A:53:TYR:CB	1:A:57:GLU:OE1	2.58	0.49
3:C:679:ILE:HG21	3:C:684:THR:HG21	1.93	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:140:ASN:HB2	3:G:141:PRO:HD3	1.94	0.49
3:G:41:ILE:HG22	3:G:44:VAL:HB	1.94	0.49
1:I:34:ILE:O	1:I:35:VAL:CG2	2.57	0.49
3:J:679:ILE:HG21	3:J:684:THR:HG21	1.93	0.49
1:A:50:LYS:HG3	1:A:51:ASP:H	1.77	0.49
1:A:168:GLY:CA	1:D:43:VAL:H	2.26	0.49
3:G:601:GLU:OE2	3:G:605:ARG:NH2	2.45	0.49
1:I:336:LYS:HE3	4:I:376:ADP:PA	2.52	0.49
1:I:50:LYS:HG3	1:I:51:ASP:H	1.77	0.49
1:A:51:ASP:O	1:A:53:TYR:CA	2.61	0.49
1:F:43:VAL:CG2	1:F:46:GLY:CA	2.90	0.49
1:F:51:ASP:O	1:F:53:TYR:CA	2.61	0.49
1:A:336:LYS:HE3	4:A:376:ADP:PA	2.52	0.49
3:C:140:ASN:HB2	3:C:141:PRO:HD3	1.94	0.49
1:E:43:VAL:CG2	1:E:46:GLY:CA	2.90	0.49
1:F:34:ILE:O	1:F:35:VAL:CG2	2.57	0.49
3:G:106:GLY:C	3:G:108:THR:N	2.63	0.49
1:D:43:VAL:CG2	1:D:46:GLY:CA	2.90	0.49
1:F:54:VAL:O	1:F:55:GLY:O	2.30	0.49
1:I:280:ASN:OD1	1:I:284:LYS:NZ	2.43	0.49
1:A:35:VAL:O	1:A:35:VAL:HG12	2.12	0.49
1:A:43:VAL:CG2	1:A:46:GLY:CA	2.90	0.49
1:D:51:ASP:O	1:D:53:TYR:CA	2.61	0.49
1:E:336:LYS:HE3	4:E:376:ADP:PA	2.52	0.48
1:E:54:VAL:O	1:E:55:GLY:O	2.30	0.48
3:J:41:ILE:HG22	3:J:44:VAL:HB	1.94	0.48
1:A:257:CYS:HB3	1:A:258:PRO:HD3	1.95	0.48
1:E:50:LYS:HG3	1:E:51:ASP:H	1.77	0.48
1:I:43:VAL:CG2	1:I:46:GLY:CA	2.90	0.48
1:A:34:ILE:O	1:A:35:VAL:CG2	2.57	0.48
3:C:601:GLU:OE2	3:C:605:ARG:NH2	2.45	0.48
1:D:73:HIC:ND1	1:D:183:ARG:HD3	2.28	0.48
1:I:53:TYR:CB	1:I:57:GLU:OE1	2.58	0.48
1:D:280:ASN:OD1	1:D:284:LYS:NZ	2.43	0.48
1:D:336:LYS:HE3	4:D:376:ADP:PA	2.52	0.48
1:F:257:CYS:HB3	1:F:258:PRO:HD3	1.95	0.48
1:F:35:VAL:HG12	1:F:35:VAL:O	2.12	0.48
3:J:55:ASN:ND2	3:J:55:ASN:O	2.47	0.48
1:E:51:ASP:O	1:E:53:TYR:CA	2.61	0.48
1:F:336:LYS:HE3	4:F:376:ADP:PA	2.52	0.48
1:F:50:LYS:HG3	1:F:51:ASP:H	1.77	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:350:SER:HB3	3:J:452:PRO:HA	1.94	0.48
1:D:35:VAL:O	1:D:35:VAL:HG12	2.12	0.48
3:G:622:ALA:HB3	3:G:678:PHE:CZ	2.49	0.48
1:I:257:CYS:HB3	1:I:258:PRO:HD3	1.95	0.48
3:C:55:ASN:ND2	3:C:55:ASN:O	2.47	0.48
3:G:327:THR:HG23	3:G:327:THR:O	2.14	0.48
3:C:369:ASN:O	3:C:373:ASN:N	2.46	0.47
3:C:622:ALA:HB3	3:C:678:PHE:CZ	2.48	0.47
1:A:66:THR:HG23	1:F:270:GLU:HG3	1.95	0.47
1:I:35:VAL:HG12	1:I:35:VAL:O	2.12	0.47
3:J:622:ALA:HB3	3:J:678:PHE:CZ	2.48	0.47
3:C:529:GLY:O	3:C:530:ASP:C	2.52	0.47
1:D:257:CYS:HB3	1:D:258:PRO:HD3	1.95	0.47
1:D:34:ILE:O	1:D:35:VAL:CG2	2.57	0.47
1:E:64:ILE:HG21	1:F:167:GLU:HG2	1.96	0.47
1:E:257:CYS:HB3	1:E:258:PRO:HD3	1.95	0.47
3:G:329:VAL:C	3:G:331:LYS:N	2.67	0.47
3:G:639:MET:SD	3:G:639:MET:N	2.87	0.47
3:J:106:GLY:C	3:J:108:THR:N	2.64	0.47
3:C:329:VAL:C	3:C:331:LYS:N	2.67	0.47
3:G:529:GLY:O	3:G:530:ASP:C	2.52	0.47
3:G:55:ASN:O	3:G:55:ASN:ND2	2.47	0.47
1:A:73:HIC:ND1	1:A:183:ARG:HD3	2.28	0.47
3:C:639:MET:N	3:C:639:MET:SD	2.87	0.47
1:I:51:ASP:O	1:I:53:TYR:CA	2.61	0.47
3:J:530:ASP:OD1	3:J:530:ASP:N	2.48	0.47
1:A:350:SER:HB3	3:C:452:PRO:HA	1.95	0.47
1:E:41:GLN:CD	1:F:170:ALA:HB3	2.32	0.47
1:E:143:TYR:OH	1:E:169:TYR:OH	2.27	0.47
1:F:42:GLY:C	1:F:44:MET:N	2.66	0.47
3:G:369:ASN:O	3:G:373:ASN:N	2.46	0.47
1:I:73:HIC:ND1	1:I:183:ARG:HD3	2.28	0.47
3:J:639:MET:SD	3:J:639:MET:N	2.87	0.47
1:A:167:GLU:HG2	1:D:64:ILE:HG21	1.96	0.47
1:E:73:HIC:ND1	1:E:183:ARG:HD3	2.28	0.47
1:A:41:GLN:NE2	1:I:170:ALA:CB	2.68	0.47
1:F:73:HIC:ND1	1:F:183:ARG:HD3	2.28	0.47
3:J:369:ASN:O	3:J:373:ASN:N	2.46	0.47
1:E:47:MET:SD	1:E:49:GLN:HA	2.55	0.47
1:E:53:TYR:CB	1:E:57:GLU:OE1	2.58	0.47
3:G:467:LYS:HE3	3:G:467:LYS:HA	1.97	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:329:VAL:C	3:J:331:LYS:N	2.67	0.47
3:J:529:GLY:O	3:J:530:ASP:C	2.52	0.47
3:J:558:ARG:HB2	3:J:559:PRO:HD3	1.96	0.47
3:C:530:ASP:OD1	3:C:530:ASP:N	2.48	0.47
2:H:222:GLU:OE1	3:J:286:GLU:CG	2.57	0.47
3:G:452:PRO:HA	1:I:350:SER:HB3	1.96	0.47
1:A:42:GLY:C	1:A:44:MET:N	2.66	0.46
1:D:1:ASP:O	1:D:2:GLU:C	2.53	0.46
3:G:624:PHE:CG	3:G:625:ALA:N	2.83	0.46
3:J:674:LYS:HG3	3:J:675:THR:HG23	1.97	0.46
1:A:47:MET:SD	1:A:49:GLN:HA	2.55	0.46
3:C:558:ARG:HB2	3:C:559:PRO:HD3	1.96	0.46
1:E:43:VAL:H	1:F:168:GLY:CA	2.29	0.46
1:I:1:ASP:O	1:I:2:GLU:C	2.54	0.46
3:C:322:TYR:HB3	3:C:337:SER:HB3	1.96	0.46
3:C:629:GLU:O	3:C:633:PHE:N	2.48	0.46
1:D:157:ASP:CB	4:D:376:ADP:O3B	2.60	0.46
1:E:203:THR:HA	1:E:206:ARG:HB3	1.97	0.46
3:G:558:ARG:HB2	3:G:559:PRO:HD3	1.96	0.46
3:J:629:GLU:O	3:J:633:PHE:N	2.48	0.46
1:A:1:ASP:O	1:A:2:GLU:C	2.54	0.46
3:C:183:LEU:HD13	3:C:184:LEU:O	2.16	0.46
1:F:47:MET:SD	1:F:49:GLN:HA	2.55	0.46
3:G:183:LEU:HD13	3:G:184:LEU:O	2.16	0.46
1:I:62:ARG:O	1:I:63:GLY:C	2.54	0.46
3:J:327:THR:O	3:J:327:THR:HG23	2.14	0.46
1:A:170:ALA:O	1:D:41:GLN:OE1	2.33	0.46
1:A:41:GLN:OE1	1:I:170:ALA:O	2.32	0.46
3:C:624:PHE:CG	3:C:625:ALA:N	2.83	0.46
3:C:674:LYS:HG3	3:C:675:THR:HG23	1.97	0.46
1:F:173:HIS:CG	1:F:174:ALA:H	2.34	0.46
3:G:629:GLU:O	3:G:633:PHE:N	2.48	0.46
3:J:634:TYR:O	3:J:636:ARG:N	2.48	0.46
1:F:203:THR:HA	1:F:206:ARG:HB3	1.97	0.46
1:F:37:ARG:CG	1:F:37:ARG:NH1	2.68	0.46
3:G:530:ASP:N	3:G:530:ASP:OD1	2.48	0.46
3:J:107:LYS:O	3:J:111:SER:HB2	2.16	0.46
1:A:173:HIS:CG	1:A:174:ALA:H	2.34	0.46
1:A:62:ARG:O	1:A:63:GLY:C	2.54	0.46
1:D:173:HIS:CG	1:D:174:ALA:H	2.34	0.46
1:F:189:LEU:HG	1:F:193:LEU:HD13	1.98	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:107:LYS:CD	3:J:107:LYS:H	2.20	0.46
3:C:467:LYS:HA	3:C:467:LYS:HE3	1.97	0.46
1:E:189:LEU:HG	1:E:193:LEU:HD13	1.98	0.46
3:G:674:LYS:HG3	3:G:675:THR:HG23	1.97	0.46
1:E:173:HIS:CG	1:E:174:ALA:H	2.34	0.46
1:I:203:THR:HA	1:I:206:ARG:HB3	1.97	0.46
3:J:624:PHE:CG	3:J:625:ALA:N	2.83	0.46
1:A:50:LYS:NZ	1:A:51:ASP:HA	2.31	0.46
1:D:62:ARG:O	1:D:63:GLY:C	2.54	0.46
1:F:50:LYS:NZ	1:F:51:ASP:HA	2.31	0.46
1:I:173:HIS:CG	1:I:174:ALA:H	2.34	0.46
3:J:106:GLY:C	3:J:108:THR:H	2.19	0.46
3:J:467:LYS:HA	3:J:467:LYS:HE3	1.97	0.46
1:A:203:THR:HA	1:A:206:ARG:HB3	1.97	0.45
1:A:41:GLN:O	1:A:43:VAL:N	2.49	0.45
3:C:573:LEU:HD22	3:C:573:LEU:O	2.16	0.45
1:E:1:ASP:O	1:E:2:GLU:C	2.53	0.45
1:E:50:LYS:NZ	1:E:51:ASP:HA	2.31	0.45
3:G:107:LYS:O	3:G:111:SER:HB2	2.16	0.45
1:I:157:ASP:CB	4:I:376:ADP:O3B	2.60	0.45
1:I:47:MET:SD	1:I:49:GLN:HA	2.55	0.45
3:J:183:LEU:HD13	3:J:184:LEU:O	2.16	0.45
3:G:573:LEU:O	3:G:573:LEU:HD22	2.16	0.45
1:D:189:LEU:HG	1:D:193:LEU:HD13	1.98	0.45
1:A:64:ILE:HG21	1:I:167:GLU:HG2	1.97	0.45
1:A:349:LEU:HD13	3:C:461:GLU:HG2	1.98	0.45
1:D:203:THR:HA	1:D:206:ARG:HB3	1.97	0.45
1:D:37:ARG:HB3	1:D:38:PRO:CD	2.47	0.45
1:F:41:GLN:O	1:F:43:VAL:N	2.49	0.45
3:G:634:TYR:O	3:G:636:ARG:N	2.48	0.45
1:E:41:GLN:O	1:E:43:VAL:N	2.49	0.45
3:G:78:TYR:CZ	3:G:81:ALA:HB2	2.52	0.45
1:I:41:GLN:O	1:I:43:VAL:N	2.49	0.45
1:I:55:GLY:C	1:I:57:GLU:N	2.58	0.45
1:A:189:LEU:HG	1:A:193:LEU:HD13	1.98	0.45
1:E:230:ALA:HA	1:E:236:LEU:HD22	1.99	0.45
1:F:1:ASP:O	1:F:2:GLU:C	2.54	0.45
3:G:470:ASP:HB3	3:G:516:VAL:HG22	1.99	0.45
1:I:37:ARG:HB3	1:I:38:PRO:CD	2.47	0.45
3:J:78:TYR:CZ	3:J:81:ALA:HB2	2.52	0.45
1:E:62:ARG:O	1:E:63:GLY:C	2.54	0.45

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:106:GLY:C	3:G:108:THR:H	2.19	0.45
1:I:50:LYS:NZ	1:I:51:ASP:HA	2.31	0.45
3:J:329:VAL:O	3:J:331:LYS:N	2.50	0.45
1:A:37:ARG:HB3	1:A:38:PRO:CD	2.47	0.45
1:E:22:ALA:N	1:E:24:ASP:OD1	2.50	0.45
1:F:230:ALA:HA	1:F:236:LEU:HD22	1.99	0.45
3:G:286:GLU:HG3	2:H:145:GLU:CD	2.37	0.45
3:C:470:ASP:HB3	3:C:516:VAL:HG22	1.99	0.45
1:D:72:GLU:O	1:D:73:HIC:C	2.65	0.45
3:J:108:THR:OG1	3:J:109:GLU:N	2.50	0.45
3:J:470:ASP:HB3	3:J:516:VAL:HG22	1.99	0.45
1:E:72:GLU:O	1:E:73:HIC:C	2.65	0.45
1:F:62:ARG:O	1:F:63:GLY:C	2.54	0.45
1:A:72:GLU:O	1:A:73:HIC:C	2.65	0.44
3:C:78:TYR:CZ	3:C:81:ALA:HB2	2.52	0.44
1:E:37:ARG:HB3	1:E:38:PRO:CD	2.47	0.44
1:F:136:ILE:HD12	1:F:136:ILE:N	2.32	0.44
1:I:72:GLU:O	1:I:73:HIC:C	2.65	0.44
3:C:456:ILE:HA	3:C:459:LEU:HB3	2.00	0.44
1:D:136:ILE:N	1:D:136:ILE:HD12	2.32	0.44
1:E:42:GLY:C	1:E:44:MET:N	2.66	0.44
1:F:22:ALA:N	1:F:24:ASP:OD1	2.50	0.44
3:G:108:THR:OG1	3:G:109:GLU:N	2.50	0.44
1:I:136:ILE:HD12	1:I:136:ILE:N	2.32	0.44
3:C:329:VAL:O	3:C:331:LYS:N	2.50	0.44
3:C:548:PRO:O	3:C:550:THR:N	2.41	0.44
3:G:19:ILE:O	3:G:19:ILE:CG2	2.65	0.44
3:G:329:VAL:O	3:G:331:LYS:N	2.50	0.44
2:H:226:LYS:HG2	3:J:285:ALA:HB1	2.00	0.44
1:I:22:ALA:N	1:I:24:ASP:OD1	2.50	0.44
3:J:456:ILE:HA	3:J:459:LEU:HB3	2.00	0.44
3:J:573:LEU:HD22	3:J:573:LEU:O	2.16	0.44
1:F:37:ARG:HB3	1:F:38:PRO:CD	2.47	0.44
1:F:72:GLU:O	1:F:73:HIC:C	2.65	0.44
3:G:456:ILE:HA	3:G:459:LEU:HB3	2.00	0.44
1:I:12:ASN:OD1	1:I:13:GLY:N	2.51	0.44
3:C:635:ASN:HA	3:C:638:LYS:HD2	2.00	0.44
1:D:12:ASN:OD1	1:D:13:GLY:N	2.51	0.44
1:D:286:ASP:O	1:D:289:ILE:HG22	2.18	0.44
1:D:41:GLN:O	1:D:43:VAL:N	2.49	0.44
3:G:288:ARG:HG3	2:H:152:LYS:NZ	2.33	0.44

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:230:ALA:HA	1:I:236:LEU:HD22	1.99	0.44
3:J:635:ASN:HA	3:J:638:LYS:HD2	2.00	0.44
1:A:136:ILE:N	1:A:136:ILE:HD12	2.32	0.44
1:A:286:ASP:O	1:A:289:ILE:HG22	2.18	0.44
1:E:12:ASN:OD1	1:E:13:GLY:N	2.51	0.44
1:E:286:ASP:O	1:E:289:ILE:HG22	2.18	0.44
1:I:189:LEU:HG	1:I:193:LEU:HD13	1.98	0.44
3:G:635:ASN:HA	3:G:638:LYS:HD2	2.00	0.44
1:A:230:ALA:HA	1:A:236:LEU:HD22	1.99	0.43
1:D:230:ALA:HA	1:D:236:LEU:HD22	1.99	0.43
1:F:12:ASN:OD1	1:F:13:GLY:N	2.51	0.43
1:F:286:ASP:O	1:F:289:ILE:HG22	2.18	0.43
2:B:199:THR:O	2:B:203:ASN:ND2	2.48	0.43
1:D:22:ALA:N	1:D:24:ASP:OD1	2.50	0.43
1:I:286:ASP:O	1:I:289:ILE:HG22	2.18	0.43
3:C:10:VAL:N	3:C:11:PRO:HD3	2.33	0.43
1:E:136:ILE:N	1:E:136:ILE:HD12	2.32	0.43
3:J:623:GLY:O	3:J:624:PHE:HB3	2.19	0.43
1:A:43:VAL:N	1:I:168:GLY:CA	2.78	0.43
3:C:623:GLY:O	3:C:624:PHE:HB3	2.19	0.43
3:C:634:TYR:O	3:C:636:ARG:N	2.48	0.43
3:G:10:VAL:N	3:G:11:PRO:HD3	2.33	0.43
3:G:623:GLY:O	3:G:624:PHE:HB3	2.19	0.43
1:A:35:VAL:HG13	1:A:52:SER:OG	2.19	0.43
1:F:35:VAL:HG13	1:F:52:SER:OG	2.19	0.43
3:J:81:ALA:O	3:J:85:TYR:N	2.52	0.43
3:C:624:PHE:CD1	3:C:624:PHE:C	2.92	0.43
1:D:148:THR:HG23	3:J:467:LYS:HB3	2.00	0.43
1:D:83:GLU:O	1:D:87:HIS:CG	2.71	0.43
1:A:12:ASN:OD1	1:A:13:GLY:N	2.51	0.43
3:C:81:ALA:O	3:C:85:TYR:N	2.52	0.43
3:J:10:VAL:N	3:J:11:PRO:HD3	2.33	0.43
1:D:42:GLY:C	1:D:44:MET:N	2.66	0.43
1:E:41:GLN:OE1	1:F:170:ALA:O	2.36	0.43
3:G:624:PHE:C	3:G:624:PHE:CD1	2.92	0.43
3:G:81:ALA:O	3:G:85:TYR:N	2.52	0.43
3:J:624:PHE:CD1	3:J:624:PHE:C	2.92	0.43
1:D:35:VAL:HG13	1:D:52:SER:OG	2.19	0.43
3:G:461:GLU:HG2	1:I:349:LEU:HD13	2.00	0.43
1:A:270:GLU:HG3	1:E:66:THR:HG23	2.01	0.42
1:D:325:MET:SD	1:D:325:MET:N	2.92	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:334:GLU:O	3:J:335:VAL:HB	2.20	0.42
3:C:334:GLU:O	3:C:335:VAL:CB	2.66	0.42
3:C:607:GLN:HA	3:C:610:TYR:CE2	2.54	0.42
3:G:607:GLN:HA	3:G:610:TYR:CE2	2.55	0.42
1:F:37:ARG:CG	1:F:38:PRO:HD3	2.47	0.42
3:J:620:ARG:CZ	3:J:620:ARG:O	2.67	0.42
1:A:157:ASP:CB	4:A:376:ADP:O3B	2.60	0.42
3:C:620:ARG:O	3:C:620:ARG:CZ	2.67	0.42
1:E:35:VAL:HG13	1:E:52:SER:OG	2.19	0.42
1:F:62:ARG:O	1:F:64:ILE:N	2.53	0.42
3:G:149:ALA:HA	3:G:200:HIS:CE1	2.55	0.42
3:G:334:GLU:O	3:G:335:VAL:HB	2.20	0.42
3:G:557:LYS:HE2	1:I:22:ALA:HB3	2.02	0.42
3:G:620:ARG:CZ	3:G:620:ARG:O	2.67	0.42
3:G:630:TYR:CD2	3:G:677:VAL:HG22	2.55	0.42
1:A:168:GLY:CA	1:D:43:VAL:N	2.81	0.42
1:A:325:MET:N	1:A:325:MET:SD	2.92	0.42
3:C:149:ALA:HA	3:C:200:HIS:CE1	2.54	0.42
3:C:630:TYR:CD2	3:C:677:VAL:HG22	2.55	0.42
1:D:202:THR:OG1	1:D:205:GLU:OE1	2.37	0.42
1:F:325:MET:SD	1:F:325:MET:N	2.92	0.42
1:A:166:TYR:HA	1:A:166:TYR:HD1	1.82	0.42
1:A:202:THR:OG1	1:A:205:GLU:OE1	2.37	0.42
1:D:375:PHE:N	1:D:375:PHE:CD1	2.88	0.42
1:E:37:ARG:HG3	1:E:38:PRO:CD	2.47	0.42
1:I:35:VAL:HG13	1:I:52:SER:OG	2.19	0.42
3:J:149:ALA:HA	3:J:200:HIS:CE1	2.54	0.42
3:J:607:GLN:HA	3:J:610:TYR:CE2	2.55	0.42
1:A:43:VAL:HG13	1:I:167:GLU:C	2.40	0.42
1:E:375:PHE:CD1	1:E:375:PHE:N	2.88	0.42
3:G:329:VAL:HG23	3:G:330:GLY:H	1.85	0.42
3:J:329:VAL:HG23	3:J:330:GLY:H	1.85	0.42
3:J:494:LYS:HA	3:J:494:LYS:HE2	2.02	0.42
1:A:375:PHE:CD1	1:A:375:PHE:N	2.87	0.41
1:D:37:ARG:CG	1:D:38:PRO:HD3	2.47	0.41
1:E:202:THR:OG1	1:E:205:GLU:OE1	2.37	0.41
1:F:287:ILE:HA	1:F:290:ARG:NH1	2.35	0.41
1:I:202:THR:OG1	1:I:205:GLU:OE1	2.37	0.41
1:E:62:ARG:O	1:E:64:ILE:N	2.53	0.41
1:F:38:PRO:HD3	1:F:49:GLN:OE1	2.21	0.41
3:J:630:TYR:CD2	3:J:677:VAL:HG22	2.55	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:229:LEU:O	3:C:232:SER:OG	2.29	0.41
1:E:157:ASP:CB	4:E:376:ADP:O3B	2.60	0.41
1:E:38:PRO:HD3	1:E:49:GLN:OE1	2.21	0.41
1:F:135:ALA:HB1	1:F:140:LEU:HD11	2.02	0.41
1:A:117:GLU:OE1	1:A:117:GLU:N	2.54	0.41
3:C:414:PHE:O	3:C:418:THR:N	2.51	0.41
1:E:135:ALA:HB1	1:E:140:LEU:HD11	2.02	0.41
1:F:202:THR:OG1	1:F:205:GLU:OE1	2.37	0.41
1:F:375:PHE:CD1	1:F:375:PHE:N	2.88	0.41
1:F:157:ASP:CB	4:F:376:ADP:O3B	2.60	0.41
3:G:414:PHE:O	3:G:418:THR:N	2.51	0.41
1:F:117:GLU:N	1:F:117:GLU:OE1	2.54	0.41
2:H:222:GLU:OE1	3:J:286:GLU:CB	2.68	0.41
1:I:171:LEU:CB	1:I:172:PRO:HD2	2.44	0.41
1:I:325:MET:SD	1:I:325:MET:N	2.92	0.41
1:I:375:PHE:CD1	1:I:375:PHE:N	2.88	0.41
1:I:42:GLY:C	1:I:44:MET:N	2.66	0.41
1:A:54:VAL:O	1:A:57:GLU:HB3	2.21	0.41
1:D:54:VAL:O	1:D:57:GLU:HB3	2.21	0.41
1:D:62:ARG:O	1:D:64:ILE:N	2.53	0.41
1:E:136:ILE:O	1:E:137:GLN:C	2.59	0.41
1:E:345:ILE:O	1:E:349:LEU:HG	2.20	0.41
3:G:223:ALA:N	3:G:224:PRO:CD	2.84	0.41
3:G:494:LYS:HE2	3:G:494:LYS:HA	2.02	0.41
1:I:62:ARG:O	1:I:64:ILE:N	2.53	0.41
1:A:6:THR:HG23	1:A:22:ALA:HB2	2.02	0.41
1:D:136:ILE:O	1:D:137:GLN:C	2.59	0.41
1:D:287:ILE:HA	1:D:290:ARG:NH1	2.36	0.41
1:A:170:ALA:CB	1:D:41:GLN:NE2	2.70	0.41
1:E:287:ILE:HA	1:E:290:ARG:NH1	2.36	0.41
3:G:181:ASN:OD1	3:G:362:ASN:ND2	2.54	0.41
3:G:417:LEU:O	3:G:421:SER:OG	2.33	0.41
3:J:79:ALA:O	3:J:83:ASP:N	2.53	0.41
1:A:62:ARG:O	1:A:64:ILE:N	2.53	0.41
3:C:181:ASN:OD1	3:C:362:ASN:ND2	2.54	0.41
3:C:498:ILE:HD12	3:C:504:ARG:HB2	2.03	0.41
3:C:532:ILE:HG23	3:C:547:PHE:CE2	2.56	0.41
3:C:79:ALA:O	3:C:83:ASP:N	2.53	0.41
1:D:171:LEU:CB	1:D:172:PRO:HD2	2.44	0.41
1:F:136:ILE:O	1:F:137:GLN:C	2.59	0.41
1:E:43:VAL:HG13	1:F:167:GLU:C	2.41	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:229:LEU:O	3:G:232:SER:OG	2.29	0.41
3:G:532:ILE:HG23	3:G:547:PHE:CE2	2.56	0.41
3:J:181:ASN:OD1	3:J:362:ASN:ND2	2.54	0.41
1:D:135:ALA:HB1	1:D:140:LEU:HD11	2.02	0.41
1:A:167:GLU:C	1:D:43:VAL:HG13	2.41	0.41
1:E:325:MET:SD	1:E:325:MET:N	2.92	0.41
2:H:222:GLU:OE1	3:J:286:GLU:CA	2.64	0.41
1:I:135:ALA:HB1	1:I:140:LEU:HD11	2.02	0.41
1:D:22:ALA:HB3	3:J:557:LYS:HE2	2.02	0.41
1:A:345:ILE:O	1:A:349:LEU:HG	2.20	0.41
1:F:163:VAL:HA	1:F:175:ILE:HG22	2.03	0.41
1:F:50:LYS:O	1:F:52:SER:N	2.54	0.41
1:I:50:LYS:O	1:I:52:SER:N	2.54	0.41
3:J:532:ILE:HG23	3:J:547:PHE:CE2	2.56	0.41
1:A:135:ALA:HB1	1:A:140:LEU:HD11	2.02	0.40
1:A:41:GLN:HE22	1:I:170:ALA:CB	2.31	0.40
3:C:621:ARG:O	3:C:622:ALA:HB2	2.21	0.40
1:D:37:ARG:HG3	1:D:38:PRO:CD	2.48	0.40
1:D:38:PRO:HD3	1:D:49:GLN:OE1	2.21	0.40
1:E:50:LYS:O	1:E:52:SER:N	2.54	0.40
3:G:79:ALA:O	3:G:83:ASP:N	2.53	0.40
1:I:287:ILE:HA	1:I:290:ARG:NH1	2.35	0.40
1:A:163:VAL:HA	1:A:175:ILE:HG22	2.03	0.40
1:A:50:LYS:O	1:A:52:SER:N	2.54	0.40
2:B:169:LEU:HD22	2:H:165:VAL:HG13	2.04	0.40
1:D:163:VAL:HA	1:D:175:ILE:HG22	2.03	0.40
1:D:345:ILE:O	1:D:349:LEU:HG	2.20	0.40
3:G:390:PHE:CZ	3:G:392:VAL:HG23	2.57	0.40
1:I:38:PRO:HD3	1:I:49:GLN:OE1	2.21	0.40
1:A:136:ILE:O	1:A:137:GLN:C	2.59	0.40
1:A:372:ARG:HA	1:A:372:ARG:CZ	2.51	0.40
1:D:372:ARG:CZ	1:D:372:ARG:HA	2.51	0.40
1:E:163:VAL:HA	1:E:175:ILE:HG22	2.03	0.40
1:E:372:ARG:HA	1:E:372:ARG:CZ	2.51	0.40
1:I:117:GLU:OE1	1:I:117:GLU:N	2.54	0.40
1:A:287:ILE:HA	1:A:290:ARG:NH1	2.36	0.40
3:C:390:PHE:CZ	3:C:392:VAL:HG23	2.57	0.40
1:E:123:MET:N	1:E:123:MET:SD	2.95	0.40
1:I:123:MET:SD	1:I:123:MET:N	2.95	0.40
3:J:223:ALA:N	3:J:224:PRO:CD	2.84	0.40
3:J:390:PHE:CZ	3:J:392:VAL:HG23	2.57	0.40

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:498:ILE:HD12	3:J:504:ARG:HB2	2.03	0.40
3:C:615:GLU:OE1	3:C:615:GLU:N	2.54	0.40
1:D:50:LYS:O	1:D:52:SER:N	2.55	0.40
1:E:54:VAL:O	1:E:57:GLU:HB3	2.21	0.40
1:F:345:ILE:O	1:F:349:LEU:HG	2.20	0.40
3:G:621:ARG:O	3:G:622:ALA:HB2	2.22	0.40
1:I:54:VAL:O	1:I:57:GLU:HB3	2.21	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	372/375 (99%)	289 (78%)	55 (15%)	28 (8%)	1	17
1	D	372/375 (99%)	288 (77%)	56 (15%)	28 (8%)	1	17
1	E	372/375 (99%)	289 (78%)	55 (15%)	28 (8%)	1	17
1	F	372/375 (99%)	289 (78%)	55 (15%)	28 (8%)	1	17
1	I	372/375 (99%)	289 (78%)	55 (15%)	28 (8%)	1	17
2	B	134/136 (98%)	134 (100%)	0	0	100	100
2	H	134/136 (98%)	134 (100%)	0	0	100	100
3	C	687/697 (99%)	574 (84%)	78 (11%)	35 (5%)	2	25
3	G	687/697 (99%)	573 (83%)	80 (12%)	34 (5%)	2	26
3	J	687/697 (99%)	574 (84%)	79 (12%)	34 (5%)	2	26
All	All	4189/4238 (99%)	3433 (82%)	513 (12%)	243 (6%)	3	23

All (243) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	42	GLY
1	A	43	VAL
1	A	47	MET
1	A	49	GLN
1	A	51	ASP
1	A	52	SER
1	A	56	ASP
1	A	63	GLY
1	A	137	GLN
3	C	59	GLU
3	C	326	SER
3	C	329	VAL
3	C	331	LYS
3	C	335	VAL
3	C	519	PHE
3	C	530	ASP
1	D	42	GLY
1	D	43	VAL
1	D	47	MET
1	D	49	GLN
1	D	51	ASP
1	D	52	SER
1	D	56	ASP
1	D	63	GLY
1	D	137	GLN
1	E	42	GLY
1	E	43	VAL
1	E	47	MET
1	E	49	GLN
1	E	51	ASP
1	E	52	SER
1	E	56	ASP
1	E	63	GLY
1	E	137	GLN
1	F	42	GLY
1	F	43	VAL
1	F	47	MET
1	F	49	GLN
1	F	51	ASP
1	F	52	SER
1	F	56	ASP
1	F	63	GLY
1	F	137	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
3	G	59	GLU
3	G	326	SER
3	G	329	VAL
3	G	331	LYS
3	G	335	VAL
3	G	519	PHE
3	G	530	ASP
1	I	42	GLY
1	I	43	VAL
1	I	47	MET
1	I	49	GLN
1	I	51	ASP
1	I	52	SER
1	I	56	ASP
1	I	63	GLY
1	I	137	GLN
3	J	59	GLU
3	J	326	SER
3	J	329	VAL
3	J	331	LYS
3	J	335	VAL
3	J	519	PHE
3	J	530	ASP
1	A	2	GLU
1	A	35	VAL
1	A	41	GLN
1	A	44	MET
1	A	48	GLY
1	A	55	GLY
1	A	167	GLU
1	A	171	LEU
1	A	173	HIS
1	A	245	GLY
3	C	42	GLY
3	C	76	HIS
3	C	92	GLN
3	C	107	LYS
3	C	283	GLU
3	C	560	GLU
3	C	622	ALA
3	C	624	PHE
1	D	2	GLU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	35	VAL
1	D	41	GLN
1	D	44	MET
1	D	48	GLY
1	D	55	GLY
1	D	167	GLU
1	D	171	LEU
1	D	173	HIS
1	D	245	GLY
1	E	2	GLU
1	E	35	VAL
1	E	41	GLN
1	E	44	MET
1	E	48	GLY
1	E	55	GLY
1	E	167	GLU
1	E	171	LEU
1	E	245	GLY
1	F	2	GLU
1	F	35	VAL
1	F	41	GLN
1	F	44	MET
1	F	48	GLY
1	F	55	GLY
1	F	167	GLU
1	F	171	LEU
1	F	173	HIS
1	F	245	GLY
3	G	42	GLY
3	G	76	HIS
3	G	92	GLN
3	G	283	GLU
3	G	560	GLU
3	G	622	ALA
3	G	624	PHE
1	I	2	GLU
1	I	35	VAL
1	I	41	GLN
1	I	44	MET
1	I	48	GLY
1	I	55	GLY
1	I	167	GLU

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	I	171	LEU
1	I	173	HIS
1	I	245	GLY
3	J	42	GLY
3	J	76	HIS
3	J	92	GLN
3	J	283	GLU
3	J	560	GLU
3	J	622	ALA
3	J	624	PHE
1	A	6	THR
1	A	38	PRO
3	C	12	ASP
3	C	380	PRO
3	C	468	SER
3	C	636	ARG
3	C	646	PRO
1	D	6	THR
1	D	38	PRO
1	E	6	THR
1	E	38	PRO
1	E	173	HIS
1	F	6	THR
1	F	38	PRO
3	G	12	ASP
3	G	380	PRO
3	G	468	SER
3	G	636	ARG
1	I	6	THR
1	I	38	PRO
3	J	12	ASP
3	J	380	PRO
3	J	468	SER
3	J	636	ARG
1	A	53	TYR
3	C	257	GLY
3	C	282	ALA
3	C	290	GLY
3	C	455	LEU
3	C	486	HIS
3	C	550	THR
3	C	551	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	53	TYR
1	E	53	TYR
1	F	53	TYR
3	G	257	GLY
3	G	282	ALA
3	G	290	GLY
3	G	455	LEU
3	G	486	HIS
3	G	550	THR
3	G	551	ARG
3	G	646	PRO
1	I	53	TYR
3	J	257	GLY
3	J	282	ALA
3	J	290	GLY
3	J	455	LEU
3	J	486	HIS
3	J	550	THR
3	J	551	ARG
3	J	646	PRO
1	A	158	GLY
1	A	172	PRO
3	C	330	GLY
3	C	524	LYS
1	D	158	GLY
1	D	172	PRO
1	E	158	GLY
1	E	172	PRO
1	F	158	GLY
1	F	172	PRO
3	G	330	GLY
3	G	524	LYS
1	I	158	GLY
1	I	172	PRO
3	J	330	GLY
3	J	524	LYS
1	A	15	GLY
1	A	70	PRO
3	C	549	PRO
3	C	635	ASN
1	D	15	GLY
1	D	70	PRO

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	E	15	GLY
1	E	70	PRO
1	F	15	GLY
1	F	70	PRO
3	G	549	PRO
3	G	635	ASN
1	I	15	GLY
1	I	70	PRO
3	J	549	PRO
3	J	635	ASN
3	C	126	SER
3	C	208	GLY
3	G	126	SER
3	G	208	GLY
3	J	126	SER
3	J	208	GLY
3	C	453	ILE
3	C	681	ASN
3	G	453	ILE
3	G	681	ASN
3	J	453	ILE
3	J	681	ASN
1	A	102	PRO
1	A	251	GLY
1	D	102	PRO
1	D	251	GLY
1	E	102	PRO
1	E	251	GLY
1	F	102	PRO
1	F	251	GLY
1	I	102	PRO
1	I	251	GLY

### 5.3.2 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 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	317/317 (100%)	289 (91%)	28 (9%)	11	37
1	D	317/317 (100%)	289 (91%)	28 (9%)	11	37
1	E	317/317 (100%)	286 (90%)	31 (10%)	9	32
1	F	317/317 (100%)	286 (90%)	31 (10%)	9	32
1	I	317/317 (100%)	286 (90%)	31 (10%)	9	32
2	B	118/118 (100%)	118 (100%)	0	100	100
2	H	118/118 (100%)	118 (100%)	0	100	100
3	C	609/616 (99%)	580 (95%)	29 (5%)	28	58
3	G	609/616 (99%)	575 (94%)	34 (6%)	23	54
3	J	609/616 (99%)	575 (94%)	34 (6%)	23	54
All	All	3648/3669 (99%)	3402 (93%)	246 (7%)	22	48

All (246) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	ARG
1	A	39	ARG
1	A	41	GLN
1	A	47	MET
1	A	49	GLN
1	A	50	LYS
1	A	52	SER
1	A	53	TYR
1	A	68	LYS
1	A	87	HIS
1	A	113	LYS
1	A	151	ILE
1	A	165	ILE
1	A	166	TYR
1	A	169	TYR
1	A	171	LEU
1	A	183	ARG
1	A	192	ILE
1	A	196	ARG
1	A	218	TYR
1	A	238	LYS
1	A	240	TYR
1	A	246	GLN
1	A	261	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	291	LYS
1	A	340	TRP
1	A	356	TRP
1	A	375	PHE
3	C	19	ILE
3	C	39	THR
3	C	54	LEU
3	C	58	LYS
3	C	91	SER
3	C	94	ASN
3	C	107	LYS
3	C	143	LEU
3	C	152	LEU
3	C	184	LEU
3	C	186	LYS
3	C	338	VAL
3	C	373	ASN
3	C	395	ASN
3	C	410	LEU
3	C	434	LYS
3	C	439	PHE
3	C	442	LYS
3	C	467	LYS
3	C	508	TYR
3	C	550	THR
3	C	551	ARG
3	C	573	LEU
3	C	620	ARG
3	C	624	PHE
3	C	636	ARG
3	C	653	LYS
3	C	667	LYS
3	C	694	LEU
1	D	2	GLU
1	D	37	ARG
1	D	39	ARG
1	D	41	GLN
1	D	49	GLN
1	D	52	SER
1	D	53	TYR
1	D	68	LYS
1	D	113	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	148	THR
1	D	151	ILE
1	D	165	ILE
1	D	166	TYR
1	D	169	TYR
1	D	171	LEU
1	D	183	ARG
1	D	192	ILE
1	D	196	ARG
1	D	218	TYR
1	D	238	LYS
1	D	240	TYR
1	D	246	GLN
1	D	261	LEU
1	D	291	LYS
1	D	326	LYS
1	D	340	TRP
1	D	356	TRP
1	D	375	PHE
1	E	2	GLU
1	E	37	ARG
1	E	39	ARG
1	E	41	GLN
1	E	47	MET
1	E	49	GLN
1	E	50	LYS
1	E	52	SER
1	E	53	TYR
1	E	68	LYS
1	E	87	HIS
1	E	113	LYS
1	E	148	THR
1	E	151	ILE
1	E	165	ILE
1	E	166	TYR
1	E	169	TYR
1	E	171	LEU
1	E	183	ARG
1	E	192	ILE
1	E	196	ARG
1	E	218	TYR
1	E	238	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	E	240	TYR
1	E	246	GLN
1	E	261	LEU
1	E	291	LYS
1	E	326	LYS
1	E	340	TRP
1	E	356	TRP
1	E	375	PHE
1	F	2	GLU
1	F	37	ARG
1	F	39	ARG
1	F	41	GLN
1	F	47	MET
1	F	49	GLN
1	F	50	LYS
1	F	52	SER
1	F	53	TYR
1	F	68	LYS
1	F	87	HIS
1	F	113	LYS
1	F	148	THR
1	F	151	ILE
1	F	165	ILE
1	F	166	TYR
1	F	169	TYR
1	F	171	LEU
1	F	183	ARG
1	F	192	ILE
1	F	196	ARG
1	F	218	TYR
1	F	238	LYS
1	F	240	TYR
1	F	246	GLN
1	F	261	LEU
1	F	291	LYS
1	F	326	LYS
1	F	340	TRP
1	F	356	TRP
1	F	375	PHE
3	G	19	ILE
3	G	39	THR
3	G	54	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
3	G	58	LYS
3	G	91	SER
3	G	94	ASN
3	G	107	LYS
3	G	143	LEU
3	G	152	LEU
3	G	184	LEU
3	G	186	LYS
3	G	288	ARG
3	G	335	VAL
3	G	336	ILE
3	G	338	VAL
3	G	373	ASN
3	G	395	ASN
3	G	410	LEU
3	G	434	LYS
3	G	439	PHE
3	G	442	LYS
3	G	467	LYS
3	G	496	ARG
3	G	508	TYR
3	G	550	THR
3	G	551	ARG
3	G	560	GLU
3	G	573	LEU
3	G	620	ARG
3	G	624	PHE
3	G	636	ARG
3	G	653	LYS
3	G	667	LYS
3	G	694	LEU
1	I	2	GLU
1	I	37	ARG
1	I	39	ARG
1	I	41	GLN
1	I	47	MET
1	I	49	GLN
1	I	50	LYS
1	I	52	SER
1	I	53	TYR
1	I	68	LYS
1	I	87	HIS

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	I	113	LYS
1	I	148	THR
1	I	151	ILE
1	I	165	ILE
1	I	166	TYR
1	I	169	TYR
1	I	171	LEU
1	I	183	ARG
1	I	192	ILE
1	I	196	ARG
1	I	218	TYR
1	I	238	LYS
1	I	240	TYR
1	I	246	GLN
1	I	261	LEU
1	I	291	LYS
1	I	326	LYS
1	I	340	TRP
1	I	356	TRP
1	I	375	PHE
3	J	19	ILE
3	J	39	THR
3	J	54	LEU
3	J	58	LYS
3	J	91	SER
3	J	94	ASN
3	J	107	LYS
3	J	143	LEU
3	J	152	LEU
3	J	184	LEU
3	J	186	LYS
3	J	288	ARG
3	J	335	VAL
3	J	336	ILE
3	J	338	VAL
3	J	373	ASN
3	J	395	ASN
3	J	410	LEU
3	J	434	LYS
3	J	439	PHE
3	J	442	LYS
3	J	467	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
3	J	496	ARG
3	J	508	TYR
3	J	550	THR
3	J	551	ARG
3	J	560	GLU
3	J	573	LEU
3	J	620	ARG
3	J	624	PHE
3	J	636	ARG
3	J	653	LYS
3	J	667	LYS
3	J	694	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	HIS
1	A	41	GLN
1	A	88	HIS
1	A	137	GLN
1	A	225	ASN
1	A	246	GLN
3	C	18	GLN
3	C	76	HIS
3	C	167	GLN
3	C	181	ASN
3	C	275	HIS
3	C	313	GLN
3	C	362	ASN
3	C	395	ASN
3	C	396	ASN
3	C	402	ASN
3	C	486	HIS
1	D	87	HIS
1	D	88	HIS
1	D	137	GLN
1	D	225	ASN
1	D	246	GLN
1	D	354	GLN
1	E	41	GLN
1	E	88	HIS
1	E	137	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	E	225	ASN
1	E	246	GLN
1	E	354	GLN
1	F	88	HIS
1	F	137	GLN
1	F	225	ASN
1	F	246	GLN
1	F	354	GLN
3	G	18	GLN
3	G	76	HIS
3	G	167	GLN
3	G	181	ASN
3	G	200	HIS
3	G	275	HIS
3	G	313	GLN
3	G	362	ASN
3	G	395	ASN
3	G	396	ASN
3	G	402	ASN
3	G	486	HIS
1	I	88	HIS
1	I	137	GLN
1	I	225	ASN
1	I	246	GLN
1	I	354	GLN
3	J	18	GLN
3	J	76	HIS
3	J	167	GLN
3	J	181	ASN
3	J	200	HIS
3	J	275	HIS
3	J	313	GLN
3	J	362	ASN
3	J	395	ASN
3	J	396	ASN
3	J	402	ASN
3	J	486	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	HIC	A	73	1	9,11,12	2.99	3 (33%)	6,14,16	2.08	3 (50%)
1	HIC	D	73	1	9,11,12	3.00	2 (22%)	6,14,16	2.07	3 (50%)
1	HIC	E	73	1	9,11,12	2.99	3 (33%)	6,14,16	2.08	3 (50%)
1	HIC	F	73	1	9,11,12	2.98	3 (33%)	6,14,16	2.08	3 (50%)
1	HIC	I	73	1	9,11,12	2.99	3 (33%)	6,14,16	2.08	3 (50%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HIC	A	73	1	-	2/4/6/8	0/1/1/1
1	HIC	D	73	1	-	2/4/6/8	0/1/1/1
1	HIC	E	73	1	-	2/4/6/8	0/1/1/1
1	HIC	F	73	1	-	2/4/6/8	0/1/1/1
1	HIC	I	73	1	-	2/4/6/8	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	73	HIC	CA-C	7.84	1.60	1.50
1	A	73	HIC	CA-C	7.81	1.60	1.50
1	I	73	HIC	CA-C	7.80	1.60	1.50
1	E	73	HIC	CA-C	7.79	1.60	1.50
1	F	73	HIC	CA-C	7.74	1.60	1.50
1	E	73	HIC	CA-N	2.68	1.56	1.47
1	I	73	HIC	CA-N	2.68	1.56	1.47
1	F	73	HIC	CA-N	2.68	1.56	1.47

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	73	HIC	CA-N	2.67	1.56	1.47
1	D	73	HIC	CA-N	2.67	1.56	1.47
1	F	73	HIC	CD2-CG	2.07	1.39	1.36
1	E	73	HIC	CD2-CG	2.05	1.39	1.36
1	A	73	HIC	CD2-CG	2.02	1.39	1.36
1	I	73	HIC	CD2-CG	2.00	1.39	1.36

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	73	HIC	CB-CA-C	-3.62	104.43	111.41
1	D	73	HIC	CB-CA-C	-3.62	104.44	111.41
1	E	73	HIC	CB-CA-C	-3.62	104.44	111.41
1	A	73	HIC	CB-CA-C	-3.61	104.45	111.41
1	F	73	HIC	CB-CA-C	-3.60	104.47	111.41
1	D	73	HIC	O-C-CA	-2.69	117.77	124.98
1	A	73	HIC	O-C-CA	-2.67	117.81	124.98
1	I	73	HIC	O-C-CA	-2.67	117.82	124.98
1	F	73	HIC	O-C-CA	-2.67	117.83	124.98
1	E	73	HIC	O-C-CA	-2.66	117.85	124.98
1	F	73	HIC	CG-CD2-NE2	-2.36	105.22	107.78
1	E	73	HIC	CG-CD2-NE2	-2.36	105.22	107.78
1	I	73	HIC	CG-CD2-NE2	-2.34	105.24	107.78
1	A	73	HIC	CG-CD2-NE2	-2.34	105.25	107.78
1	D	73	HIC	CG-CD2-NE2	-2.30	105.29	107.78

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	73	HIC	N-CA-CB-CG
1	D	73	HIC	C-CA-CB-CG
1	A	73	HIC	N-CA-CB-CG
1	A	73	HIC	C-CA-CB-CG
1	I	73	HIC	N-CA-CB-CG
1	I	73	HIC	C-CA-CB-CG
1	F	73	HIC	N-CA-CB-CG
1	F	73	HIC	C-CA-CB-CG
1	E	73	HIC	N-CA-CB-CG
1	E	73	HIC	C-CA-CB-CG

There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	73	HIC	2	0
1	D	73	HIC	2	0
1	E	73	HIC	2	0
1	F	73	HIC	2	0
1	I	73	HIC	2	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
4	ADP	A	376	-	24,29,29	1.13	1 (4%)	25,45,45	1.45	4 (16%)
4	ADP	D	376	-	24,29,29	1.13	1 (4%)	25,45,45	1.44	4 (16%)
4	ADP	E	376	-	24,29,29	1.12	1 (4%)	25,45,45	1.45	4 (16%)
4	ADP	F	376	-	24,29,29	1.13	1 (4%)	25,45,45	1.45	4 (16%)
4	ADP	I	376	-	24,29,29	1.13	2 (8%)	25,45,45	1.46	4 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ADP	A	376	-	-	0/12/32/32	0/3/3/3
4	ADP	D	376	-	-	0/12/32/32	0/3/3/3
4	ADP	E	376	-	-	0/12/32/32	0/3/3/3
4	ADP	F	376	-	-	0/12/32/32	0/3/3/3

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ADP	I	376	-	-	0/12/32/32	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	376	ADP	C2-N1	2.97	1.39	1.33
4	D	376	ADP	C2-N1	2.95	1.39	1.33
4	I	376	ADP	C2-N1	2.94	1.39	1.33
4	F	376	ADP	C2-N1	2.93	1.39	1.33
4	E	376	ADP	C2-N1	2.89	1.39	1.33
4	I	376	ADP	C8-N7	-2.00	1.31	1.34

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	376	ADP	C4-C5-N7	3.96	113.52	109.40
4	I	376	ADP	C4-C5-N7	3.94	113.50	109.40
4	F	376	ADP	C4-C5-N7	3.92	113.49	109.40
4	A	376	ADP	C4-C5-N7	3.89	113.45	109.40
4	D	376	ADP	C4-C5-N7	3.87	113.43	109.40
4	I	376	ADP	C2-N1-C6	2.17	122.52	118.77
4	A	376	ADP	C2-N1-C6	2.15	122.50	118.77
4	F	376	ADP	C2-N1-C6	2.14	122.48	118.77
4	A	376	ADP	N3-C2-N1	-2.14	125.23	128.68
4	E	376	ADP	C2-N1-C6	2.14	122.47	118.77
4	I	376	ADP	N3-C2-N1	-2.13	125.25	128.68
4	D	376	ADP	C2-N1-C6	2.13	122.45	118.77
4	F	376	ADP	N3-C2-N1	-2.12	125.26	128.68
4	D	376	ADP	N3-C2-N1	-2.12	125.26	128.68
4	E	376	ADP	N3-C2-N1	-2.10	125.30	128.68
4	A	376	ADP	O3B-PB-O2B	2.09	115.71	107.57
4	F	376	ADP	O3B-PB-O2B	2.08	115.67	107.57
4	D	376	ADP	O3B-PB-O2B	2.08	115.66	107.57
4	E	376	ADP	O3B-PB-O2B	2.08	115.66	107.57
4	I	376	ADP	O3B-PB-O2B	2.07	115.61	107.57

There are no chirality outliers.

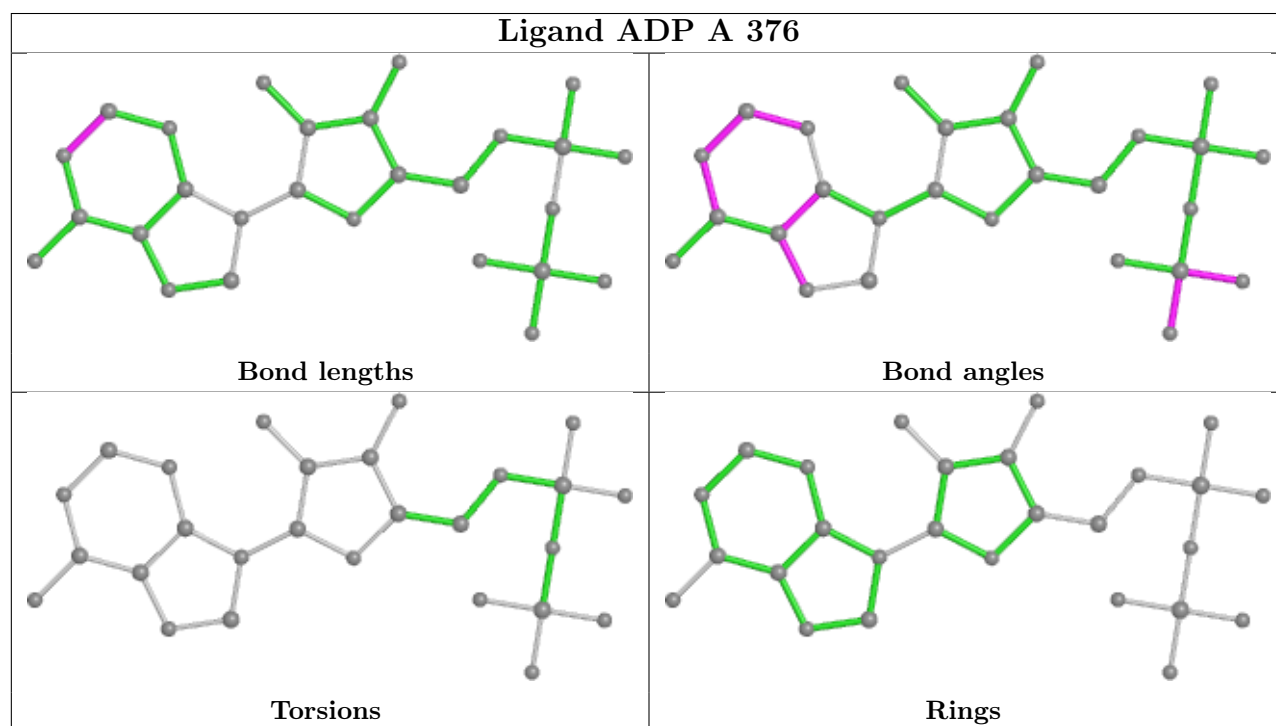
There are no torsion outliers.

There are no ring outliers.

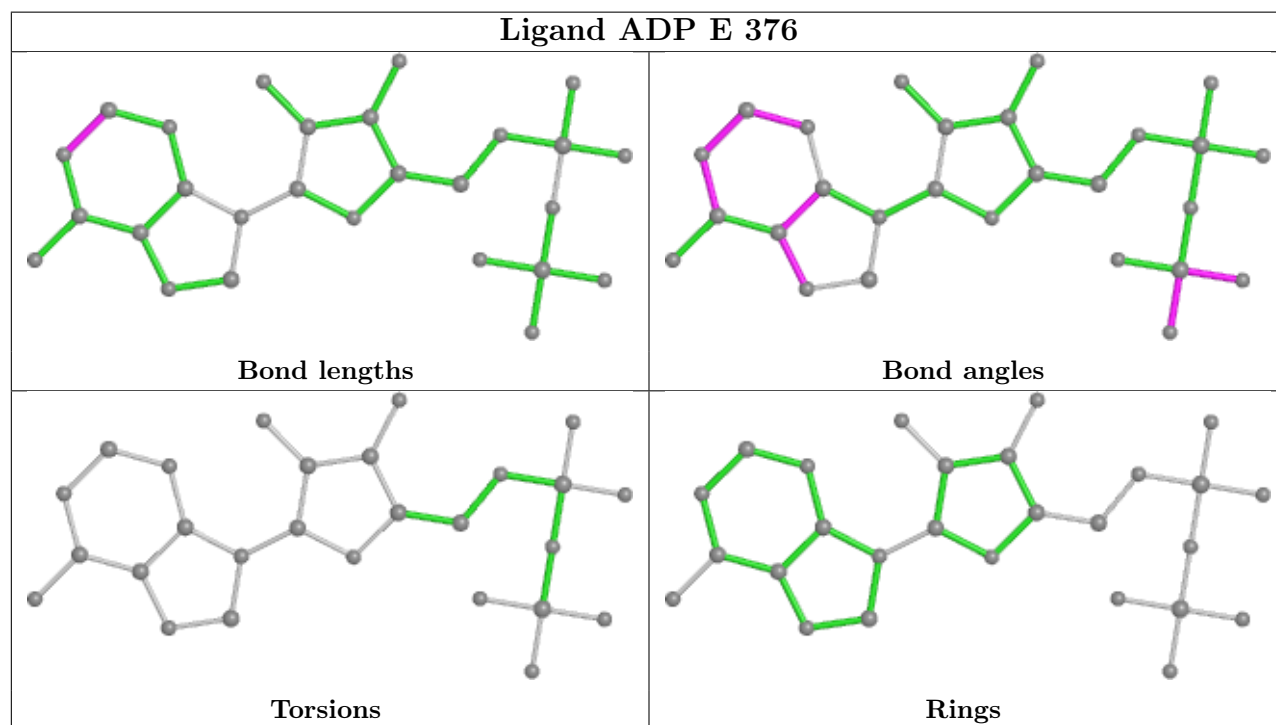
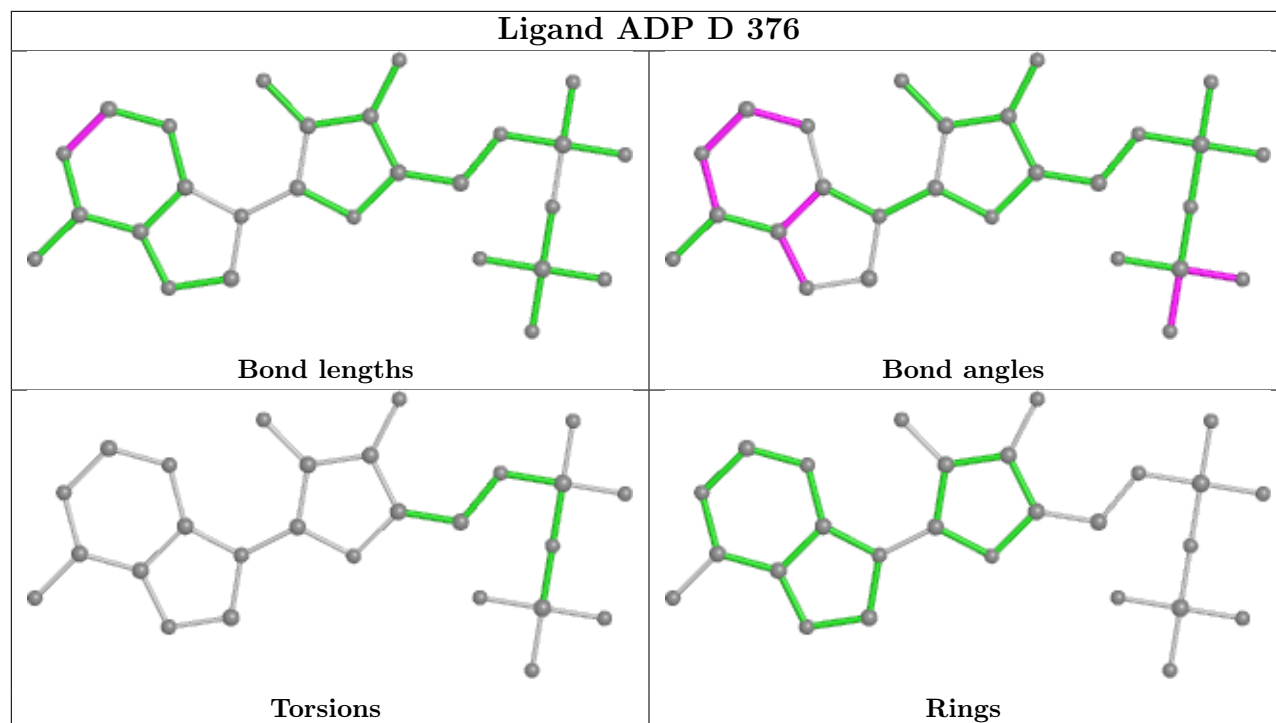
5 monomers are involved in 20 short contacts:

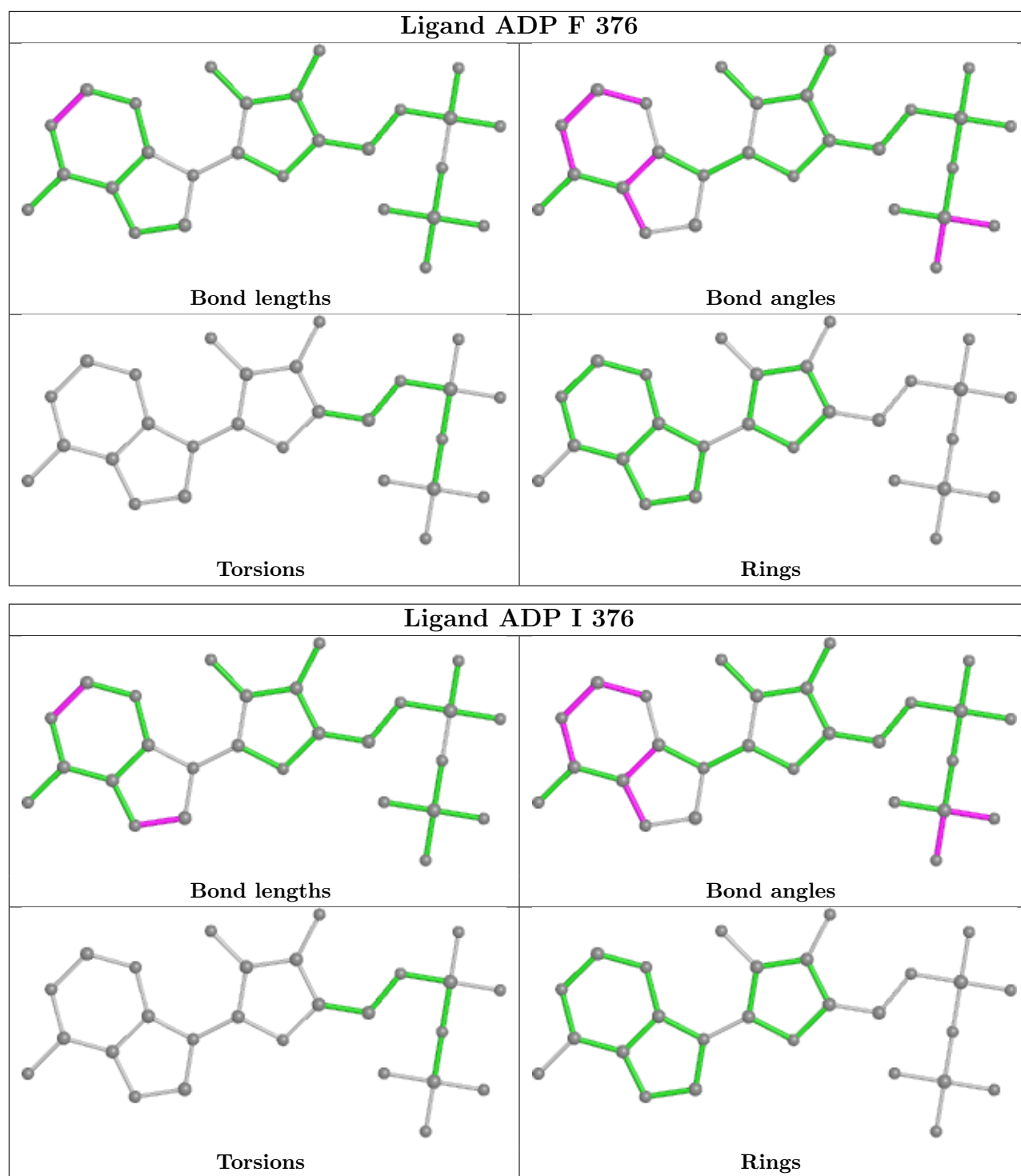
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	376	ADP	4	0
4	D	376	ADP	4	0
4	E	376	ADP	4	0
4	F	376	ADP	4	0
4	I	376	ADP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.