



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:36 AM GMT

PDB ID : 3PCC
Title : STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COM-
PLEXED WITH 4-HYDROXYBENZOATE
Authors : Elango, N.; Orville, A.M.; Lipscomb, J.D.; Ohlendorf, D.H.
Deposited on : 1997-04-29
Resolution : 1.98 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
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) : trunk26865

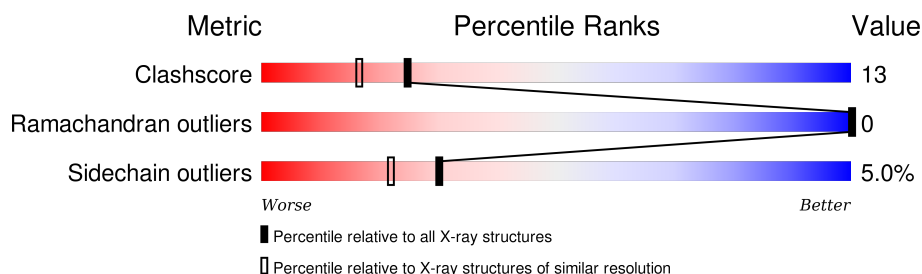
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.98 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	9905 (2.00-1.96)
Ramachandran outliers	100387	9792 (2.00-1.96)
Sidechain outliers	100360	9791 (2.00-1.96)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	200	 73% 24% ..
1	B	200	 69% 25% 6% .
1	C	200	 72% 24% ..
1	D	200	 71% 24% 5%
1	E	200	 69% 25% 6% .
1	F	200	 65% 30% 6%
2	M	238	 77% 17% ..

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	N	238	<div><div></div><div>75%</div><div>21%</div><div></div><div>...</div></div>
2	O	238	<div><div></div><div>75%</div><div>19%</div><div></div><div>..</div></div>
2	P	238	<div><div></div><div>76%</div><div>18%</div><div></div><div>...</div></div>
2	Q	238	<div><div></div><div>72%</div><div>21%</div><div></div><div>...</div></div>
2	R	238	<div><div></div><div>71%</div><div>22%</div><div>5%</div><div></div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 22062 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 PROTOCATECHUATE 3,4-DIOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	200	Total	C	N	O	S	0	0	0
			1571	993	276	299	3			
1	B	200	Total	C	N	O	S	0	0	0
			1571	993	276	299	3			
1	C	200	Total	C	N	O	S	0	0	0
			1571	993	276	299	3			
1	D	200	Total	C	N	O	S	0	0	0
			1571	993	276	299	3			
1	E	200	Total	C	N	O	S	0	0	0
			1571	993	276	299	3			
1	F	200	Total	C	N	O	S	0	0	0
			1571	993	276	299	3			

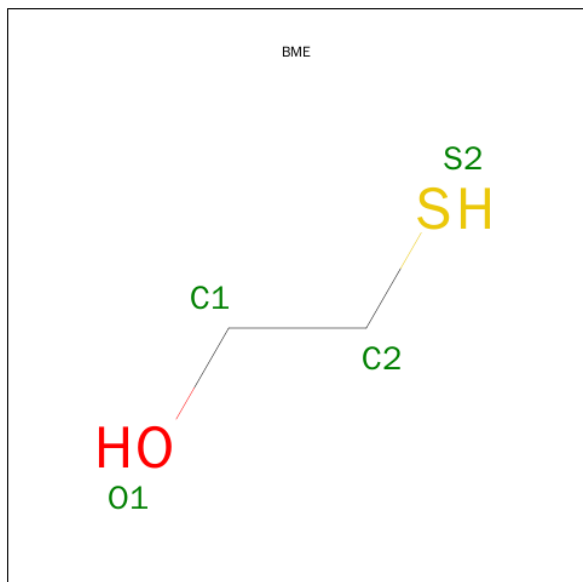
- Molecule 2 is a protein called PROTOCATECHUATE 3,4-DIOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	233	Total	C	N	O	S	0	0	0
			1840	1171	334	328	7			
2	N	233	Total	C	N	O	S	0	0	0
			1840	1171	334	328	7			
2	O	233	Total	C	N	O	S	0	0	0
			1840	1171	334	328	7			
2	P	233	Total	C	N	O	S	0	0	0
			1840	1171	334	328	7			
2	Q	233	Total	C	N	O	S	0	0	0
			1840	1171	334	328	7			
2	R	233	Total	C	N	O	S	0	0	0
			1840	1171	334	328	7			

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

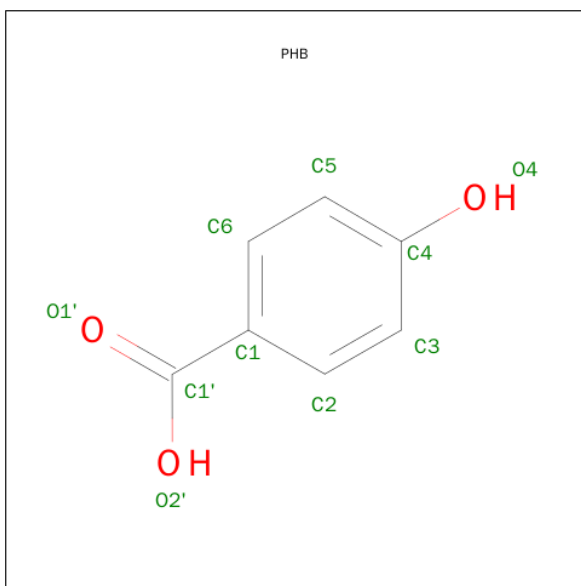
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	P	1	Total Fe 1 1	0	0
3	Q	1	Total Fe 1 1	0	0
3	N	1	Total Fe 1 1	0	0
3	O	1	Total Fe 1 1	0	0
3	R	1	Total Fe 1 1	0	0
3	M	1	Total Fe 1 1	0	0

- Molecule 4 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	M	1	Total C O S 4 2 1 1	0	0
4	N	1	Total C O S 4 2 1 1	0	0
4	O	1	Total C O S 4 2 1 1	0	0
4	P	1	Total C O S 4 2 1 1	0	0
4	Q	1	Total C O S 4 2 1 1	0	0
4	R	1	Total C O S 4 2 1 1	0	0

- Molecule 5 is P-HYDROXYBENZOIC ACID (three-letter code: PHB) (formula: $C_7H_6O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	M	1	Total	C	O	0	0
			10	7	3		
5	M	1	Total	C	O	0	0
			10	7	3		
5	N	1	Total	C	O	0	0
			10	7	3		
5	N	1	Total	C	O	0	0
			10	7	3		
5	O	1	Total	C	O	0	0
			10	7	3		
5	O	1	Total	C	O	0	0
			10	7	3		
5	P	1	Total	C	O	0	0
			10	7	3		
5	P	1	Total	C	O	0	0
			10	7	3		
5	Q	1	Total	C	O	0	0
			10	7	3		
5	Q	1	Total	C	O	0	0
			10	7	3		
5	R	1	Total	C	O	0	0
			10	7	3		
5	R	1	Total	C	O	0	0
			10	7	3		

- Molecule 6 is water.

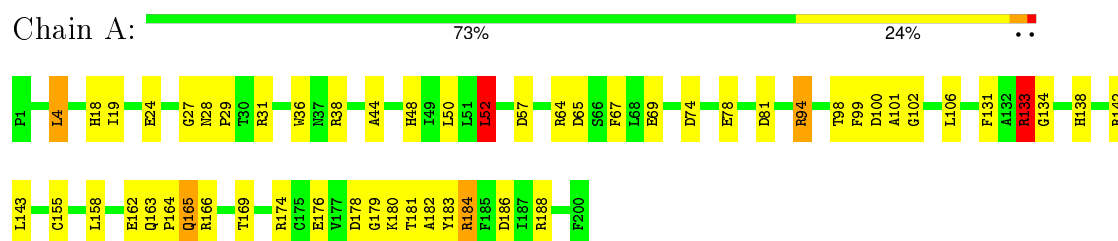
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	81	Total 81	O 81	0	0
6	B	82	Total 82	O 82	0	0
6	C	82	Total 82	O 82	0	0
6	D	83	Total 83	O 83	0	0
6	E	87	Total 87	O 87	0	0
6	F	74	Total 74	O 74	0	0
6	M	160	Total 160	O 160	0	0
6	N	162	Total 162	O 162	0	0
6	O	159	Total 159	O 159	0	0
6	P	151	Total 151	O 151	0	0
6	Q	157	Total 157	O 157	0	0
6	R	168	Total 168	O 168	0	0

3 Residue-property plots

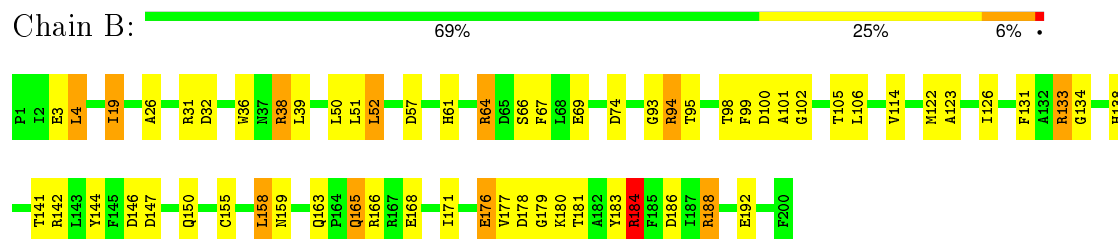
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

Note EDS was not executed.

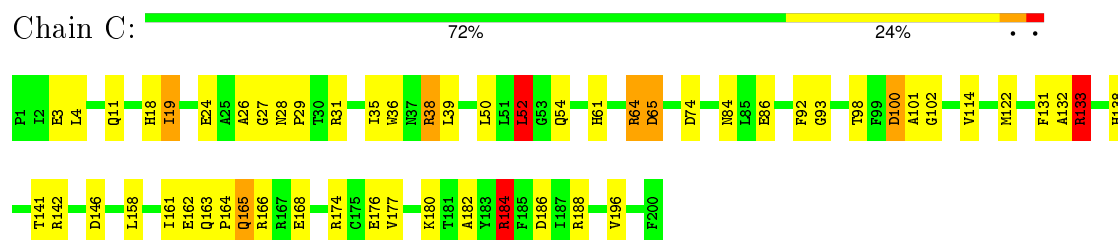
• Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE



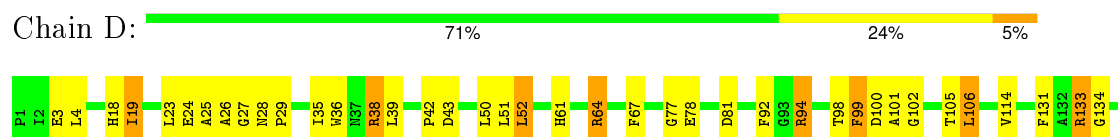
• Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE



• Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE



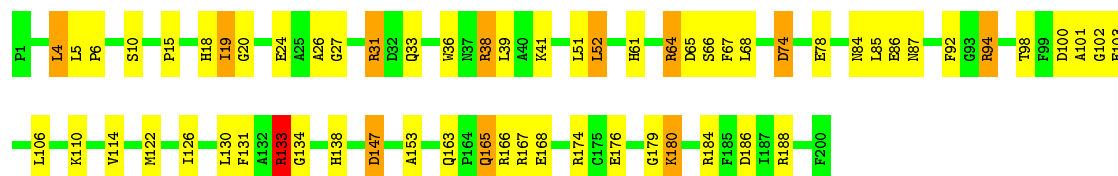
• Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE





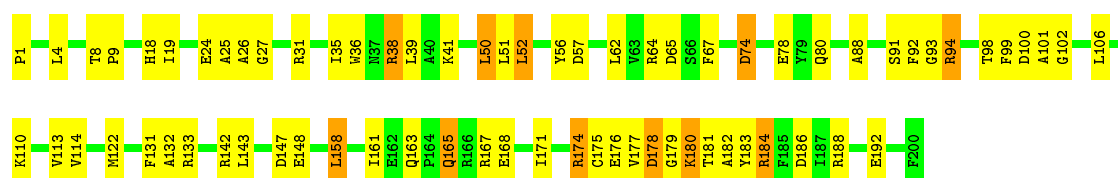
• Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE

Chain E: 69% 25% 6%



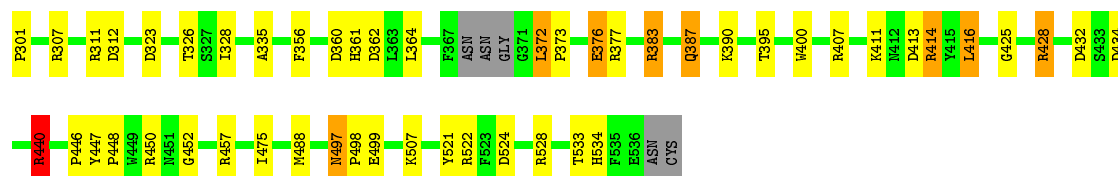
• Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE

Chain F: 65% 30% 6%



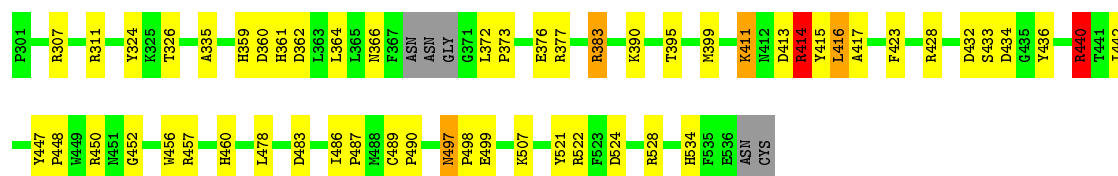
• Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE

Chain M: 77% 17% 6%



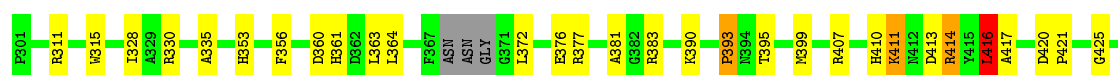
• Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE

Chain N: 75% 21% 4%



• Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE

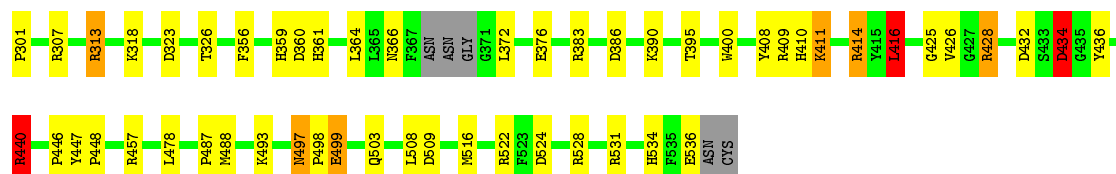
Chain O: 75% 19% 6%





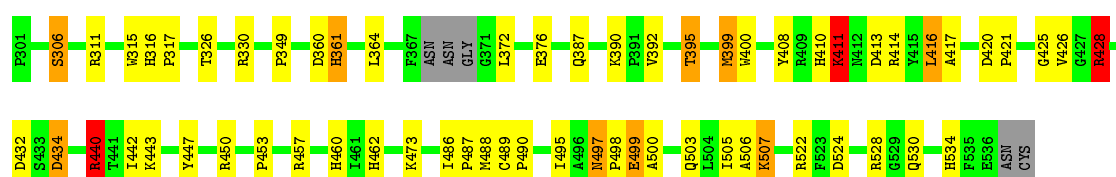
• Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE

Chain P: 76% 18% . . .



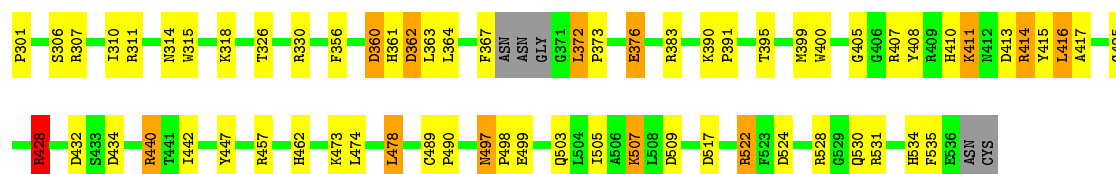
• Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE

Chain Q: 72% 21% . . .



• Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE

Chain R: 71% 22% 5% .



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	197.41Å 127.97Å 134.88Å 90.00° 97.80° 90.00°	Depositor
Resolution (Å)	6.00 – 1.98	Depositor
% Data completeness (in resolution range)	67.7 (6.00-1.98)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.163 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	22062	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PHB, FE, BME

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 > 5$	RMSZ	# $ Z > 5$
1	A	1.02	2/1611 (0.1%)	1.73	30/2195 (1.4%)
1	B	1.04	1/1611 (0.1%)	1.71	28/2195 (1.3%)
1	C	1.06	0/1611	1.53	28/2195 (1.3%)
1	D	1.05	1/1611 (0.1%)	1.63	19/2195 (0.9%)
1	E	1.10	2/1611 (0.1%)	1.63	21/2195 (1.0%)
1	F	1.07	1/1611 (0.1%)	1.68	30/2195 (1.4%)
2	M	1.14	3/1895 (0.2%)	1.70	35/2580 (1.4%)
2	N	1.14	3/1895 (0.2%)	1.71	29/2580 (1.1%)
2	O	1.14	1/1895 (0.1%)	1.66	35/2580 (1.4%)
2	P	1.10	2/1895 (0.1%)	1.62	32/2580 (1.2%)
2	Q	1.13	2/1895 (0.1%)	1.68	27/2580 (1.0%)
2	R	1.08	1/1895 (0.1%)	1.64	30/2580 (1.2%)
All	All	1.09	19/21036 (0.1%)	1.66	344/28650 (1.2%)

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	B	0	1
1	C	0	1
1	F	0	1
All	All	0	3

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	94	ARG	CD-NE	-9.62	1.30	1.46
1	E	94	ARG	CD-NE	-8.56	1.31	1.46
1	D	94	ARG	CD-NE	-7.29	1.34	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Q	428	ARG	CD-NE	-6.79	1.34	1.46
2	O	428	ARG	CD-NE	-6.29	1.35	1.46
2	R	428	ARG	CD-NE	-6.20	1.35	1.46
2	M	452	GLY	CA-C	6.15	1.61	1.51
2	P	428	ARG	CD-NE	-5.95	1.36	1.46
2	N	428	ARG	CD-NE	-5.88	1.36	1.46
2	P	440	ARG	CD-NE	-5.83	1.36	1.46
1	B	94	ARG	CG-CD	-5.77	1.37	1.51
2	Q	306	SER	CA-CB	5.76	1.61	1.52
1	E	10	SER	CA-CB	5.75	1.61	1.52
2	N	428	ARG	CG-CD	-5.63	1.37	1.51
2	M	440	ARG	CD-NE	-5.55	1.37	1.46
1	F	94	ARG	CD-NE	-5.46	1.37	1.46
2	M	428	ARG	CD-NE	-5.15	1.37	1.46
2	N	324	TYR	CE1-CZ	5.02	1.45	1.38
1	A	94	ARG	CG-CD	-5.00	1.39	1.51

All (344) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	ARG	CD-NE-CZ	27.95	162.73	123.60
2	M	440	ARG	NE-CZ-NH2	-24.58	108.01	120.30
2	N	440	ARG	NE-CZ-NH2	-24.05	108.27	120.30
2	P	440	ARG	NE-CZ-NH2	-23.32	108.64	120.30
2	Q	440	ARG	NE-CZ-NH2	-21.15	109.72	120.30
2	O	440	ARG	NE-CZ-NH2	-21.01	109.79	120.30
2	Q	440	ARG	NE-CZ-NH1	19.17	129.88	120.30
2	N	428	ARG	NE-CZ-NH1	18.81	129.70	120.30
1	B	94	ARG	NE-CZ-NH1	17.68	129.14	120.30
1	E	94	ARG	NE-CZ-NH1	17.63	129.12	120.30
2	Q	428	ARG	CD-NE-CZ	17.25	147.75	123.60
2	R	440	ARG	NE-CZ-NH2	-16.54	112.03	120.30
1	F	94	ARG	NE-CZ-NH1	15.75	128.17	120.30
1	D	94	ARG	NE-CZ-NH1	15.56	128.08	120.30
1	E	94	ARG	CG-CD-NE	15.35	144.04	111.80
1	A	94	ARG	CG-CD-NE	15.33	143.99	111.80
1	D	94	ARG	CD-NE-CZ	15.28	145.00	123.60
2	O	428	ARG	CD-NE-CZ	15.27	144.98	123.60
2	R	428	ARG	CD-NE-CZ	14.69	144.16	123.60
1	E	94	ARG	CD-NE-CZ	14.63	144.09	123.60
1	F	94	ARG	CD-NE-CZ	14.56	143.99	123.60
1	D	94	ARG	NE-CZ-NH2	-13.98	113.31	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	428	ARG	NE-CZ-NH1	13.78	127.19	120.30
1	B	184	ARG	NE-CZ-NH2	-13.63	113.48	120.30
1	A	94	ARG	NE-CZ-NH1	13.63	127.12	120.30
1	E	94	ARG	NE-CZ-NH2	-12.80	113.90	120.30
1	F	94	ARG	NE-CZ-NH2	-12.75	113.92	120.30
2	M	383	ARG	NE-CZ-NH1	-12.33	114.14	120.30
2	R	428	ARG	NE-CZ-NH1	12.29	126.44	120.30
2	O	414	ARG	NE-CZ-NH1	-12.25	114.18	120.30
1	D	166	ARG	NE-CZ-NH1	12.16	126.38	120.30
1	B	94	ARG	NE-CZ-NH2	-12.15	114.23	120.30
1	B	133	ARG	CD-NE-CZ	12.08	140.51	123.60
1	D	38	ARG	NE-CZ-NH2	-12.07	114.27	120.30
2	N	428	ARG	NE-CZ-NH2	-12.06	114.27	120.30
2	Q	457	ARG	NE-CZ-NH2	-11.94	114.33	120.30
2	O	450	ARG	NE-CZ-NH1	11.62	126.11	120.30
2	Q	428	ARG	NE-CZ-NH2	-11.61	114.49	120.30
2	M	440	ARG	NE-CZ-NH1	11.58	126.09	120.30
2	Q	457	ARG	NE-CZ-NH1	11.43	126.01	120.30
1	F	133	ARG	NE-CZ-NH1	11.36	125.98	120.30
2	N	311	ARG	NE-CZ-NH1	11.29	125.94	120.30
2	N	428	ARG	CD-NE-CZ	11.24	139.33	123.60
1	C	133	ARG	NE-CZ-NH2	-11.10	114.75	120.30
2	M	428	ARG	NE-CZ-NH1	10.87	125.74	120.30
1	B	166	ARG	NE-CZ-NH1	10.86	125.73	120.30
1	D	38	ARG	NE-CZ-NH1	10.85	125.72	120.30
2	N	428	ARG	CG-CD-NE	10.64	134.15	111.80
2	M	428	ARG	NE-CZ-NH2	-10.54	115.03	120.30
2	O	428	ARG	NE-CZ-NH2	-10.52	115.04	120.30
1	B	188	ARG	NE-CZ-NH1	10.50	125.55	120.30
2	P	440	ARG	NE-CZ-NH1	10.41	125.50	120.30
1	A	94	ARG	NE-CZ-NH2	-10.40	115.10	120.30
2	R	428	ARG	CG-CD-NE	10.39	133.63	111.80
2	N	457	ARG	NE-CZ-NH2	-10.29	115.16	120.30
1	B	133	ARG	NE-CZ-NH1	10.17	125.39	120.30
2	Q	428	ARG	NE-CZ-NH1	10.14	125.37	120.30
1	B	94	ARG	CB-CG-CD	10.11	137.89	111.60
2	N	450	ARG	NE-CZ-NH2	-10.08	115.26	120.30
2	P	428	ARG	NE-CZ-NH2	-9.95	115.32	120.30
2	R	428	ARG	NE-CZ-NH2	-9.84	115.38	120.30
2	R	307	ARG	NE-CZ-NH1	9.77	125.18	120.30
1	C	133	ARG	NE-CZ-NH1	9.73	125.16	120.30
2	O	428	ARG	CG-CD-NE	9.68	132.12	111.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	133	ARG	NE-CZ-NH2	-9.62	115.49	120.30
2	R	440	ARG	NE-CZ-NH1	9.62	125.11	120.30
1	E	38	ARG	NE-CZ-NH1	9.62	125.11	120.30
1	B	184	ARG	NE-CZ-NH1	9.61	125.11	120.30
1	F	142	ARG	NE-CZ-NH1	9.60	125.10	120.30
2	M	428	ARG	CD-NE-CZ	9.53	136.94	123.60
1	E	38	ARG	NE-CZ-NH2	-9.46	115.57	120.30
2	R	522	ARG	NE-CZ-NH1	-9.41	115.59	120.30
1	D	94	ARG	CG-CD-NE	9.25	131.23	111.80
2	O	450	ARG	NE-CZ-NH2	-9.22	115.69	120.30
2	M	522	ARG	NE-CZ-NH1	-9.16	115.72	120.30
1	F	186	ASP	CB-CG-OD1	9.13	126.52	118.30
2	M	311	ARG	NE-CZ-NH2	-9.11	115.75	120.30
2	R	432	ASP	CB-CG-OD2	-9.11	110.11	118.30
1	C	188	ARG	NE-CZ-NH1	9.01	124.80	120.30
1	B	94	ARG	CG-CD-NE	8.96	130.60	111.80
2	R	457	ARG	NE-CZ-NH2	-8.89	115.86	120.30
2	M	457	ARG	CD-NE-CZ	8.81	135.93	123.60
2	P	409	ARG	NE-CZ-NH1	8.76	124.68	120.30
1	A	142	ARG	NE-CZ-NH1	8.74	124.67	120.30
2	N	528	ARG	NE-CZ-NH2	-8.73	115.94	120.30
2	M	312	ASP	CB-CG-OD1	8.70	126.13	118.30
1	B	188	ARG	NE-CZ-NH2	-8.70	115.95	120.30
1	A	184	ARG	NE-CZ-NH2	-8.61	116.00	120.30
2	P	457	ARG	NE-CZ-NH1	8.61	124.61	120.30
2	N	311	ARG	NE-CZ-NH2	-8.48	116.06	120.30
1	F	133	ARG	NE-CZ-NH2	-8.45	116.08	120.30
2	P	428	ARG	CG-CD-NE	8.43	129.51	111.80
1	F	94	ARG	CG-CD-NE	8.41	129.45	111.80
1	F	167	ARG	NE-CZ-NH2	-8.25	116.17	120.30
2	N	450	ARG	CD-NE-CZ	8.19	135.07	123.60
1	E	31	ARG	NE-CZ-NH2	-8.14	116.23	120.30
2	O	432	ASP	CB-CG-OD1	8.11	125.60	118.30
2	N	428	ARG	CB-CG-CD	8.08	132.62	111.60
2	Q	311	ARG	CD-NE-CZ	8.06	134.88	123.60
1	A	94	ARG	CB-CG-CD	8.03	132.48	111.60
2	M	407	ARG	NE-CZ-NH1	8.03	124.31	120.30
2	N	440	ARG	NE-CZ-NH1	7.98	124.29	120.30
1	B	31	ARG	NE-CZ-NH1	7.95	124.28	120.30
2	P	386	ASP	CB-CG-OD2	7.94	125.45	118.30
2	R	528	ARG	NE-CZ-NH1	-7.92	116.34	120.30
1	C	74	ASP	CB-CG-OD1	7.90	125.41	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	524	ASP	CB-CG-OD1	7.89	125.40	118.30
1	E	186	ASP	CB-CG-OD1	7.87	125.38	118.30
1	B	146	ASP	CB-CG-OD1	7.84	125.36	118.30
1	C	31	ARG	NE-CZ-NH2	-7.81	116.40	120.30
1	C	174	ARG	NE-CZ-NH2	-7.78	116.41	120.30
2	Q	432	ASP	CB-CG-OD2	-7.74	111.34	118.30
2	N	307	ARG	NE-CZ-NH1	7.72	124.16	120.30
2	R	414	ARG	NE-CZ-NH2	-7.69	116.45	120.30
1	D	166	ARG	NE-CZ-NH2	-7.62	116.49	120.30
1	F	188	ARG	NE-CZ-NH2	-7.62	116.49	120.30
2	M	457	ARG	NE-CZ-NH1	7.61	124.10	120.30
1	A	57	ASP	CB-CG-OD1	7.55	125.10	118.30
2	O	434	ASP	CB-CG-OD2	-7.54	111.52	118.30
2	O	383	ARG	NE-CZ-NH2	-7.52	116.54	120.30
1	F	184	ARG	NE-CZ-NH2	-7.48	116.56	120.30
2	O	457	ARG	NE-CZ-NH2	-7.47	116.56	120.30
1	C	142	ARG	NE-CZ-NH1	7.46	124.03	120.30
2	M	414	ARG	NE-CZ-NH1	7.46	124.03	120.30
2	Q	428	ARG	CG-CD-NE	7.46	127.46	111.80
2	N	521	TYR	CB-CG-CD2	-7.46	116.53	121.00
2	P	383	ARG	NE-CZ-NH1	-7.45	116.58	120.30
2	M	450	ARG	NE-CZ-NH1	7.40	124.00	120.30
1	A	184	ARG	NE-CZ-NH1	7.39	124.00	120.30
1	C	184	ARG	NE-CZ-NH1	7.36	123.98	120.30
1	A	133	ARG	NE-CZ-NH2	7.36	123.98	120.30
2	N	440	ARG	NH1-CZ-NH2	7.29	127.42	119.40
1	E	133	ARG	CD-NE-CZ	-7.28	113.41	123.60
1	A	166	ARG	NE-CZ-NH1	7.26	123.93	120.30
2	N	450	ARG	NE-CZ-NH1	7.24	123.92	120.30
1	A	31	ARG	NE-CZ-NH1	7.22	123.91	120.30
2	P	522	ARG	NE-CZ-NH1	-7.22	116.69	120.30
1	C	166	ARG	NE-CZ-NH1	7.20	123.90	120.30
2	O	414	ARG	CD-NE-CZ	-7.20	113.52	123.60
2	N	524	ASP	CB-CG-OD2	-7.12	111.89	118.30
2	P	524	ASP	CB-CG-OD1	7.09	124.68	118.30
2	R	531	ARG	NE-CZ-NH1	7.09	123.85	120.30
2	M	414	ARG	NE-CZ-NH2	-7.08	116.76	120.30
1	F	133	ARG	CD-NE-CZ	7.08	133.51	123.60
2	O	528	ARG	NE-CZ-NH2	-7.07	116.77	120.30
1	B	192	GLU	CA-CB-CG	7.07	128.95	113.40
2	O	440	ARG	NE-CZ-NH1	7.03	123.82	120.30
2	M	428	ARG	CG-CD-NE	7.03	126.56	111.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	65	ASP	CB-CG-OD1	7.02	124.61	118.30
1	B	95	THR	CA-CB-CG2	7.01	122.21	112.40
2	Q	450	ARG	NE-CZ-NH2	-6.99	116.81	120.30
1	F	38	ARG	NE-CZ-NH2	-6.97	116.82	120.30
1	B	142	ARG	NE-CZ-NH2	-6.91	116.84	120.30
2	R	383	ARG	NE-CZ-NH2	-6.90	116.85	120.30
2	R	509	ASP	CB-CG-OD2	-6.88	112.11	118.30
2	O	432	ASP	CB-CG-OD2	-6.87	112.12	118.30
1	E	166	ARG	NE-CZ-NH2	-6.85	116.87	120.30
2	O	455	ASP	CB-CG-OD2	-6.85	112.14	118.30
1	F	188	ARG	NE-CZ-NH1	6.81	123.70	120.30
2	Q	528	ARG	NE-CZ-NH2	-6.80	116.90	120.30
2	R	376	GLU	CG-CD-OE2	-6.78	104.74	118.30
2	R	517	ASP	CB-CG-OD1	6.77	124.39	118.30
2	P	531	ARG	NE-CZ-NH1	6.77	123.68	120.30
2	P	509	ASP	CB-CG-OD2	-6.73	112.25	118.30
2	R	457	ARG	CA-CB-CG	6.73	128.20	113.40
2	P	313	ARG	NE-CZ-NH1	6.72	123.66	120.30
1	E	166	ARG	NE-CZ-NH1	6.72	123.66	120.30
1	C	38	ARG	CD-NE-CZ	-6.70	114.22	123.60
1	C	100	ASP	CB-CG-OD2	6.68	124.31	118.30
2	M	432	ASP	CB-CG-OD1	6.67	124.31	118.30
2	O	407	ARG	NE-CZ-NH1	6.67	123.63	120.30
1	A	57	ASP	CB-CG-OD2	-6.66	112.31	118.30
2	N	434	ASP	CB-CG-OD2	-6.65	112.31	118.30
2	Q	360	ASP	CB-CG-OD2	-6.65	112.31	118.30
2	Q	434	ASP	CB-CG-OD2	-6.65	112.31	118.30
1	F	94	ARG	CB-CG-CD	6.64	128.86	111.60
2	R	407	ARG	NE-CZ-NH1	6.63	123.62	120.30
1	C	168	GLU	OE1-CD-OE2	6.62	131.24	123.30
2	O	377	ARG	NE-CZ-NH1	6.58	123.59	120.30
2	M	323	ASP	CB-CG-OD2	-6.58	112.38	118.30
1	D	133	ARG	NE-CZ-NH2	6.57	123.58	120.30
2	P	524	ASP	CB-CG-OD2	-6.57	112.39	118.30
1	D	142	ARG	NE-CZ-NH1	-6.55	117.03	120.30
1	A	31	ARG	NE-CZ-NH2	-6.54	117.03	120.30
2	P	499	GLU	CA-CB-CG	6.51	127.72	113.40
1	D	167	ARG	NE-CZ-NH1	6.46	123.53	120.30
1	B	186	ASP	CB-CG-OD2	-6.45	112.49	118.30
1	F	167	ARG	CD-NE-CZ	-6.43	114.59	123.60
2	Q	360	ASP	CB-CG-OD1	6.39	124.05	118.30
2	P	323	ASP	CB-CG-OD1	6.38	124.04	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	36	TRP	CB-CA-C	6.34	123.09	110.40
2	N	432	ASP	CB-CG-OD2	-6.34	112.60	118.30
2	P	440	ARG	CD-NE-CZ	6.34	132.47	123.60
2	R	522	ARG	NE-CZ-NH2	6.32	123.46	120.30
2	M	521	TYR	CB-CG-CD1	-6.29	117.23	121.00
2	O	330	ARG	NE-CZ-NH2	-6.28	117.16	120.30
2	P	383	ARG	CD-NE-CZ	-6.24	114.86	123.60
2	N	311	ARG	CD-NE-CZ	6.21	132.29	123.60
2	Q	372	LEU	CA-CB-CG	6.20	129.57	115.30
1	B	36	TRP	CB-CA-C	6.20	122.80	110.40
1	C	158	LEU	CB-CA-C	6.19	121.95	110.20
1	F	38	ARG	NE-CZ-NH1	6.19	123.39	120.30
2	Q	432	ASP	CB-CG-OD1	6.17	123.86	118.30
1	C	100	ASP	CB-CG-OD1	-6.15	112.77	118.30
1	F	186	ASP	CB-CG-OD2	-6.14	112.77	118.30
1	D	23	LEU	CB-CA-C	6.14	121.86	110.20
2	M	312	ASP	CB-CG-OD2	-6.13	112.79	118.30
2	P	432	ASP	CB-CG-OD1	6.12	123.81	118.30
1	F	65	ASP	CB-CG-OD2	-6.12	112.79	118.30
2	R	376	GLU	OE1-CD-OE2	6.12	130.65	123.30
1	F	36	TRP	CB-CA-C	6.11	122.61	110.40
1	A	162	GLU	OE1-CD-OE2	6.10	130.62	123.30
1	C	3	GLU	OE1-CD-OE2	6.10	130.62	123.30
1	E	52	LEU	CB-CA-C	6.10	121.79	110.20
2	R	311	ARG	NE-CZ-NH2	-6.10	117.25	120.30
2	R	307	ARG	NE-CZ-NH2	-6.09	117.26	120.30
1	D	64	ARG	CD-NE-CZ	-6.08	115.09	123.60
2	O	428	ARG	CB-CG-CD	6.07	127.39	111.60
2	P	307	ARG	NE-CZ-NH1	6.07	123.34	120.30
2	Q	311	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	A	188	ARG	NE-CZ-NH2	-6.04	117.28	120.30
2	O	499	GLU	CG-CD-OE1	6.04	130.37	118.30
2	O	440	ARG	NH1-CZ-NH2	6.00	126.00	119.40
1	E	64	ARG	CD-NE-CZ	-5.99	115.21	123.60
2	Q	524	ASP	CB-CG-OD1	5.99	123.69	118.30
1	F	174	ARG	NE-CZ-NH2	-5.98	117.31	120.30
2	P	531	ARG	NE-CZ-NH2	-5.97	117.31	120.30
2	Q	440	ARG	CD-NE-CZ	5.96	131.95	123.60
2	O	450	ARG	CD-NE-CZ	5.92	131.89	123.60
2	M	524	ASP	CB-CG-OD1	5.92	123.63	118.30
1	C	52	LEU	CB-CA-C	5.91	121.43	110.20
1	C	64	ARG	NE-CZ-NH1	-5.89	117.35	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	457	ARG	NE-CZ-NH1	5.88	123.24	120.30
2	P	536	GLU	CA-C-O	5.88	132.45	120.10
1	C	11	GLN	N-CA-CB	5.87	121.16	110.60
2	R	311	ARG	NE-CZ-NH1	5.84	123.22	120.30
2	P	457	ARG	CD-NE-CZ	5.81	131.74	123.60
1	A	74	ASP	CB-CG-OD2	-5.79	113.09	118.30
1	C	141	THR	CA-CB-CG2	5.79	120.51	112.40
1	D	52	LEU	CB-CA-C	5.79	121.20	110.20
2	Q	411	LYS	CB-CA-C	-5.79	98.83	110.40
1	F	192	GLU	OE1-CD-OE2	5.78	130.24	123.30
1	A	186	ASP	CB-CG-OD2	-5.78	113.10	118.30
1	B	178	ASP	CB-CG-OD2	5.78	123.50	118.30
2	M	383	ARG	NH1-CZ-NH2	5.76	125.73	119.40
2	N	360	ASP	CB-CG-OD2	-5.76	113.12	118.30
1	D	43	ASP	CB-CG-OD2	-5.75	113.13	118.30
1	A	52	LEU	CB-CA-C	5.74	121.10	110.20
1	B	64	ARG	NE-CZ-NH2	-5.73	117.44	120.30
2	O	360	ASP	CB-CG-OD2	-5.73	113.14	118.30
1	B	57	ASP	CB-CG-OD1	5.69	123.42	118.30
1	E	31	ARG	NE-CZ-NH1	5.67	123.13	120.30
1	E	36	TRP	CB-CA-C	5.66	121.71	110.40
1	A	188	ARG	NE-CZ-NH1	5.65	123.12	120.30
2	M	323	ASP	CB-CG-OD1	5.63	123.37	118.30
1	E	147	ASP	CB-CG-OD1	5.60	123.34	118.30
1	A	36	TRP	CB-CA-C	5.60	121.59	110.40
2	N	377	ARG	NE-CZ-NH2	-5.59	117.51	120.30
1	A	81	ASP	CB-CG-OD2	-5.57	113.29	118.30
2	P	372	LEU	CB-CA-C	5.57	120.77	110.20
2	P	313	ARG	NE-CZ-NH2	-5.56	117.52	120.30
2	Q	506	ALA	CB-CA-C	5.56	118.44	110.10
1	C	64	ARG	CD-NE-CZ	-5.55	115.83	123.60
1	C	3	GLU	CG-CD-OE1	-5.55	107.21	118.30
1	D	36	TRP	CB-CA-C	5.54	121.49	110.40
2	O	353	HIS	CA-CB-CG	-5.54	104.18	113.60
1	C	166	ARG	NE-CZ-NH2	-5.53	117.53	120.30
2	N	452	GLY	N-CA-C	-5.53	99.28	113.10
1	B	38	ARG	CD-NE-CZ	-5.52	115.87	123.60
1	C	168	GLU	CG-CD-OE2	-5.51	107.28	118.30
1	F	158	LEU	CB-CA-C	5.51	120.67	110.20
2	M	522	ARG	NE-CZ-NH2	5.51	123.06	120.30
2	O	414	ARG	NE-CZ-NH2	5.50	123.05	120.30
2	P	434	ASP	CB-CG-OD1	-5.49	113.36	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	168	GLU	CG-CD-OE2	-5.48	107.33	118.30
1	B	94	ARG	CD-NE-CZ	5.47	131.26	123.60
1	E	167	ARG	NE-CZ-NH2	5.46	123.03	120.30
1	A	174	ARG	NE-CZ-NH1	5.45	123.02	120.30
2	R	407	ARG	NE-CZ-NH2	-5.45	117.58	120.30
2	O	524	ASP	CB-CG-OD1	5.44	123.19	118.30
2	P	428	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	E	153	ALA	CB-CA-C	5.43	118.24	110.10
1	C	65	ASP	CB-CG-OD1	5.42	123.18	118.30
1	A	178	ASP	CB-CG-OD1	5.42	123.18	118.30
2	O	416	LEU	CB-CA-C	5.42	120.50	110.20
2	Q	528	ARG	NE-CZ-NH1	5.40	123.00	120.30
2	M	411	LYS	CB-CA-C	-5.38	99.64	110.40
2	O	440	ARG	O-C-N	5.38	131.31	122.70
2	P	440	ARG	NH1-CZ-NH2	5.38	125.31	119.40
2	Q	361	HIS	CA-CB-CG	-5.36	104.48	113.60
2	O	440	ARG	CB-CG-CD	-5.34	97.70	111.60
1	F	175	CYS	CA-CB-SG	5.34	123.62	114.00
1	F	74	ASP	CB-CG-OD2	-5.32	113.51	118.30
1	C	186	ASP	CB-CG-OD1	5.31	123.08	118.30
2	N	434	ASP	OD1-CG-OD2	5.31	133.39	123.30
1	D	81	ASP	CB-CG-OD1	5.30	123.07	118.30
2	R	360	ASP	CB-CG-OD1	5.30	123.07	118.30
2	P	528	ARG	NE-CZ-NH2	-5.30	117.65	120.30
2	M	376	GLU	OE1-CD-OE2	5.29	129.65	123.30
1	D	186	ASP	CB-CG-OD2	-5.28	113.54	118.30
2	R	367	PHE	CA-C-O	-5.28	109.01	120.10
1	A	186	ASP	CB-CG-OD1	5.25	123.03	118.30
2	M	383	ARG	CD-NE-CZ	-5.25	116.25	123.60
1	C	146	ASP	CB-CG-OD1	5.25	123.02	118.30
2	P	434	ASP	CA-CB-CG	-5.24	101.87	113.40
2	M	440	ARG	NH1-CZ-NH2	5.22	125.14	119.40
2	M	432	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	B	4	LEU	N-CA-CB	-5.21	99.97	110.40
2	M	528	ARG	CD-NE-CZ	5.21	130.89	123.60
2	N	457	ARG	NE-CZ-NH1	5.20	122.90	120.30
2	Q	330	ARG	NE-CZ-NH2	-5.19	117.71	120.30
2	M	376	GLU	CG-CD-OE2	-5.18	107.93	118.30
2	M	428	ARG	CB-CG-CD	5.18	125.08	111.60
2	R	362	ASP	CB-CG-OD2	5.18	122.96	118.30
1	F	52	LEU	CA-CB-CG	5.17	127.19	115.30
2	M	387	GLN	N-CA-CB	5.17	119.90	110.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	57	ASP	CB-CG-OD2	-5.17	113.65	118.30
1	A	183	TYR	N-CA-CB	5.16	119.89	110.60
1	B	66	SER	N-CA-CB	5.16	118.24	110.50
2	O	335	ALA	CB-CA-C	-5.16	102.36	110.10
1	A	69	GLU	OE1-CD-OE2	-5.16	117.11	123.30
2	O	311	ARG	CD-NE-CZ	5.15	130.81	123.60
2	P	416	LEU	CB-CA-C	5.15	119.98	110.20
1	E	74	ASP	CB-CG-OD1	5.13	122.92	118.30
2	N	483	ASP	CB-CG-OD2	5.12	122.91	118.30
2	M	440	ARG	CD-NE-CZ	5.12	130.77	123.60
1	E	52	LEU	CA-CB-CG	5.12	127.07	115.30
2	N	383	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	A	81	ASP	CB-CG-OD1	5.11	122.90	118.30
2	N	414	ARG	NE-CZ-NH1	5.10	122.85	120.30
2	R	478	LEU	CA-CB-CG	5.09	127.02	115.30
2	Q	473	LYS	CD-CE-NZ	-5.09	99.99	111.70
2	Q	306	SER	CB-CA-C	-5.08	100.44	110.10
1	C	162	GLU	CA-CB-CG	5.08	124.57	113.40
1	B	158	LEU	CA-CB-CG	5.07	126.97	115.30
2	M	452	GLY	N-CA-C	-5.07	100.43	113.10
1	A	166	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	D	99	PHE	N-CA-CB	5.06	119.71	110.60
1	F	31	ARG	NE-CZ-NH2	-5.03	117.78	120.30
2	O	417	ALA	CB-CA-C	5.02	117.63	110.10
2	P	416	LEU	CA-CB-CG	5.02	126.85	115.30
1	B	69	GLU	OE1-CD-OE2	-5.01	117.29	123.30
1	F	52	LEU	CB-CA-C	5.01	119.71	110.20
1	A	169	THR	CA-CB-CG2	5.00	119.41	112.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	188	ARG	Sidechain
1	C	184	ARG	Sidechain
1	F	184	ARG	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	1571	0	1499	40	0
1	B	1571	0	1499	47	0
1	C	1571	0	1499	45	0
1	D	1571	0	1499	45	0
1	E	1571	0	1499	51	0
1	F	1571	0	1499	65	0
2	M	1840	0	1792	40	0
2	N	1840	0	1792	38	0
2	O	1840	0	1792	38	0
2	P	1840	0	1792	46	0
2	Q	1840	0	1792	55	0
2	R	1840	0	1792	55	0
3	M	1	0	0	0	0
3	N	1	0	0	0	0
3	O	1	0	0	0	0
3	P	1	0	0	0	0
3	Q	1	0	0	0	0
3	R	1	0	0	0	0
4	M	4	0	5	0	0
4	N	4	0	5	0	0
4	O	4	0	5	0	0
4	P	4	0	5	0	0
4	Q	4	0	5	0	0
4	R	4	0	5	0	0
5	M	20	0	9	0	0
5	N	20	0	9	1	0
5	O	20	0	9	0	0
5	P	20	0	8	0	0
5	Q	20	0	9	0	0
5	R	20	0	9	1	0
6	A	81	0	0	1	0
6	B	82	0	0	1	0
6	C	82	0	0	1	0
6	D	83	0	0	0	0
6	E	87	0	0	1	0
6	F	74	0	0	1	0
6	M	160	0	0	2	0
6	N	162	0	0	3	0
6	O	159	0	0	3	0
6	P	151	0	0	2	0
6	Q	157	0	0	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	R	168	0	0	4	0
All	All	22062	0	19829	519	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 13.

All (519) 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:N:411:LYS:N	2:N:411:LYS:HE2	1.31	1.37
1:C:26:ALA:O	2:O:411:LYS:NZ	1.61	1.31
2:N:411:LYS:H	2:N:411:LYS:CE	1.43	1.31
2:P:411:LYS:HE2	2:P:411:LYS:N	1.49	1.26
2:P:411:LYS:H	2:P:411:LYS:CE	1.56	1.18
1:F:64:ARG:NH1	1:F:100:ASP:O	1.77	1.18
1:C:64:ARG:NH1	1:C:100:ASP:O	1.83	1.11
1:E:26:ALA:O	2:Q:411:LYS:NZ	1.86	1.07
1:E:64:ARG:NH1	1:E:100:ASP:O	1.88	1.07
1:A:98:THR:HB	1:A:100:ASP:OD1	1.56	1.05
1:E:165:GLN:NE2	1:E:165:GLN:H	1.56	1.04
1:B:26:ALA:O	2:N:411:LYS:NZ	1.91	1.02
1:F:26:ALA:O	2:R:411:LYS:NZ	1.93	1.02
1:E:98:THR:HB	1:E:100:ASP:OD1	1.61	1.01
1:B:98:THR:HB	1:B:100:ASP:OD1	1.62	0.99
1:F:98:THR:HB	1:F:100:ASP:OD1	1.62	0.98
1:E:165:GLN:N	1:E:165:GLN:HE21	1.62	0.95
1:B:163:GLN:HB3	1:B:165:GLN:HE22	1.31	0.95
1:B:165:GLN:NE2	1:B:165:GLN:H	1.63	0.94
1:F:163:GLN:HB3	1:F:165:GLN:NE2	1.83	0.94
1:D:26:ALA:O	2:P:411:LYS:HE3	1.68	0.93
1:F:163:GLN:HB3	1:F:165:GLN:HE22	1.32	0.92
2:M:497:ASN:HD22	2:M:499:GLU:H	1.16	0.92
1:B:163:GLN:HB3	1:B:165:GLN:NE2	1.87	0.90
1:D:98:THR:OG1	1:D:102:GLY:N	2.05	0.90
2:N:390:LYS:HD3	6:N:747:HOH:O	1.71	0.90
1:C:163:GLN:HB3	1:C:165:GLN:NE2	1.88	0.88
1:D:26:ALA:O	2:P:411:LYS:CE	2.21	0.87
1:A:98:THR:OG1	1:A:102:GLY:N	2.08	0.87
2:Q:411:LYS:H	2:Q:411:LYS:CE	1.88	0.87
1:D:165:GLN:H	1:D:165:GLN:NE2	1.70	0.87
2:R:411:LYS:CE	2:R:411:LYS:H	1.89	0.86

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:64:ARG:NH1	1:B:100:ASP:O	2.09	0.85
1:D:165:GLN:H	1:D:165:GLN:HE21	1.20	0.85
2:P:411:LYS:O	2:P:414:ARG:NH1	2.10	0.84
1:A:163:GLN:HB3	1:A:165:GLN:NE2	1.91	0.84
1:B:26:ALA:O	2:N:411:LYS:CE	2.26	0.84
2:R:361:HIS:H	2:R:361:HIS:CD2	1.93	0.83
2:N:497:ASN:HD22	2:N:499:GLU:H	1.27	0.83
2:R:390:LYS:HE2	6:R:873:HOH:O	1.78	0.82
1:D:64:ARG:NH1	1:D:100:ASP:O	2.13	0.81
1:C:54:GLN:HG3	1:C:184:ARG:NH2	1.96	0.81
2:O:411:LYS:CE	2:O:411:LYS:H	1.93	0.80
2:Q:361:HIS:H	2:Q:361:HIS:CD2	1.96	0.79
1:F:174:ARG:HE	1:F:181:THR:HG21	1.47	0.79
1:C:26:ALA:O	2:O:411:LYS:CE	2.30	0.78
2:Q:390:LYS:HD2	6:Q:663:HOH:O	1.82	0.78
1:F:174:ARG:HE	1:F:181:THR:CG2	1.97	0.78
1:D:64:ARG:HG2	1:D:64:ARG:HH11	1.45	0.78
1:F:168:GLU:HA	1:F:171:ILE:HD12	1.65	0.78
1:D:98:THR:HB	1:D:100:ASP:OD1	1.85	0.77
1:F:78:GLU:HG2	2:R:301:PRO:HG2	1.63	0.77
1:F:177:VAL:O	1:F:180:LYS:HB3	1.85	0.77
2:M:497:ASN:ND2	2:M:499:GLU:H	1.84	0.76
1:D:64:ARG:NH1	1:D:64:ARG:HG2	2.01	0.76
2:O:411:LYS:H	2:O:411:LYS:HE2	1.50	0.75
1:C:100:ASP:CG	1:C:101:ALA:H	1.90	0.75
1:B:67:PHE:HZ	1:B:94:ARG:HD2	1.52	0.74
2:Q:361:HIS:H	2:Q:361:HIS:HD2	1.31	0.74
2:P:364:LEU:HD22	2:P:440:ARG:HD3	1.69	0.74
1:E:176:GLU:OE2	1:E:179:GLY:HA2	1.86	0.74
2:M:361:HIS:H	2:M:361:HIS:CD2	2.04	0.74
2:Q:411:LYS:H	2:Q:411:LYS:HE2	1.50	0.74
1:A:67:PHE:HZ	1:A:94:ARG:HD2	1.53	0.74
2:P:313:ARG:O	2:P:318:LYS:HE3	1.88	0.73
1:E:98:THR:OG1	1:E:102:GLY:N	2.22	0.73
1:D:24:GLU:O	1:D:27:GLY:N	2.21	0.73
1:F:24:GLU:O	1:F:27:GLY:N	2.21	0.73
1:B:176:GLU:HG3	1:B:180:LYS:O	1.89	0.73
1:D:153:ALA:HB3	1:D:154:LYS:HE3	1.71	0.72
2:R:361:HIS:H	2:R:361:HIS:HD2	1.34	0.72
1:F:110:LYS:NZ	1:F:148:GLU:OE2	2.17	0.72
1:A:163:GLN:HB2	6:A:819:HOH:O	1.89	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:67:PHE:HZ	1:E:94:ARG:HD2	1.56	0.71
2:N:361:HIS:H	2:N:361:HIS:CD2	2.08	0.71
1:F:165:GLN:NE2	1:F:165:GLN:H	1.89	0.71
1:E:176:GLU:HG3	1:E:180:LYS:O	1.91	0.70
2:R:497:ASN:ND2	2:R:499:GLU:H	1.90	0.70
1:A:163:GLN:HB3	1:A:165:GLN:HE22	1.56	0.70
1:A:176:GLU:HG2	1:A:179:GLY:HA2	1.72	0.70
1:F:100:ASP:CG	1:F:101:ALA:H	1.95	0.70
2:R:497:ASN:HD22	2:R:499:GLU:H	1.39	0.70
1:F:163:GLN:CB	1:F:165:GLN:HE22	2.04	0.69
2:N:497:ASN:ND2	2:N:499:GLU:H	1.91	0.69
2:P:376:GLU:OE1	6:P:675:HOH:O	2.11	0.69
1:C:163:GLN:HB3	1:C:165:GLN:HE22	1.58	0.69
1:E:147:ASP:OD2	1:E:174:ARG:NH1	2.25	0.69
2:Q:416:LEU:C	2:Q:416:LEU:HD23	2.13	0.68
2:O:361:HIS:CD2	2:O:361:HIS:H	2.09	0.68
2:P:361:HIS:CD2	2:P:361:HIS:H	2.12	0.68
2:O:413:ASP:C	2:O:414:ARG:HD2	2.14	0.68
1:C:165:GLN:H	1:C:165:GLN:NE2	1.91	0.67
2:R:315:TRP:HZ2	2:R:503:GLN:HE21	1.43	0.67
1:F:64:ARG:HD3	1:F:99:PHE:O	1.93	0.67
2:R:411:LYS:H	2:R:411:LYS:HE2	1.60	0.67
2:Q:497:ASN:ND2	2:Q:499:GLU:HB2	2.10	0.66
2:N:497:ASN:ND2	2:N:499:GLU:HB2	2.10	0.66
1:E:24:GLU:O	1:E:27:GLY:N	2.27	0.66
1:F:98:THR:OG1	1:F:102:GLY:N	2.28	0.66
1:A:165:GLN:H	1:A:165:GLN:CD	1.98	0.66
1:C:24:GLU:O	1:C:27:GLY:N	2.28	0.66
1:B:165:GLN:N	1:B:165:GLN:NE2	2.43	0.66
1:F:165:GLN:CD	1:F:165:GLN:H	1.98	0.66
1:E:65:ASP:OD2	1:E:133:ARG:HD3	1.96	0.66
2:O:390:LYS:HE2	6:O:798:HOH:O	1.94	0.66
1:F:50:LEU:HD12	1:F:51:LEU:N	2.11	0.65
1:A:67:PHE:CZ	1:A:94:ARG:HD2	2.31	0.65
1:E:26:ALA:O	2:Q:411:LYS:CE	2.43	0.65
2:P:411:LYS:HE2	2:P:411:LYS:H	0.64	0.65
1:D:165:GLN:N	1:D:165:GLN:HE21	1.94	0.65
2:N:383:ARG:HG3	2:N:436:TYR:CE1	2.32	0.65
2:M:356:PHE:HD1	2:M:428:ARG:HD3	1.62	0.65
1:A:64:ARG:NH1	1:A:100:ASP:O	2.31	0.64
2:N:361:HIS:HD2	2:N:361:HIS:H	1.44	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:67:PHE:CZ	1:B:94:ARG:HD2	2.31	0.64
2:R:505:ILE:HG22	2:R:507:LYS:HE2	1.79	0.64
1:C:54:GLN:HG3	1:C:184:ARG:HH21	1.62	0.64
2:R:522:ARG:NH1	6:R:814:HOH:O	2.29	0.64
1:C:98:THR:OG1	1:C:102:GLY:N	2.30	0.64
1:A:100:ASP:CG	1:A:101:ALA:H	2.01	0.64
1:B:168:GLU:HA	1:B:171:ILE:HD12	1.79	0.64
1:B:26:ALA:O	2:N:411:LYS:HE3	1.98	0.63
1:E:51:LEU:HD12	1:E:106:LEU:HD23	1.79	0.63
2:M:364:LEU:HD22	2:M:440:ARG:HD3	1.81	0.63
1:A:176:GLU:HG3	1:A:180:LYS:O	1.98	0.63
2:Q:505:ILE:O	2:Q:507:LYS:HE3	1.99	0.63
1:E:61:HIS:ND1	1:F:163:GLN:HG3	2.13	0.63
1:E:110:LYS:NZ	1:E:147:ASP:OD1	2.29	0.62
2:Q:497:ASN:HD22	2:Q:499:GLU:H	1.45	0.62
1:D:67:PHE:HZ	1:D:94:ARG:HD2	1.63	0.62
2:N:390:LYS:HE2	6:N:828:HOH:O	1.99	0.62
2:Q:411:LYS:H	2:Q:411:LYS:NZ	1.98	0.62
1:B:165:GLN:HE21	1:B:165:GLN:H	1.48	0.62
1:E:165:GLN:H	1:E:165:GLN:HE21	0.77	0.61
2:Q:497:ASN:ND2	2:Q:499:GLU:H	1.98	0.61
1:D:67:PHE:CZ	1:D:94:ARG:HD2	2.34	0.61
2:R:410:HIS:HA	2:R:411:LYS:NZ	2.15	0.61
1:F:177:VAL:HG12	1:F:178:ASP:OD2	2.01	0.61
2:M:361:HIS:HD2	2:M:361:HIS:H	1.47	0.61
1:B:134:GLY:HA3	2:N:326:THR:HG22	1.81	0.61
2:M:448:PRO:HB2	2:P:516:MET:HA	1.82	0.61
2:Q:315:TRP:HZ2	2:Q:503:GLN:HE21	1.48	0.60
1:C:98:THR:HB	1:C:100:ASP:OD1	2.02	0.60
1:F:176:GLU:HG2	1:F:179:GLY:HA2	1.83	0.60
2:Q:411:LYS:N	2:Q:411:LYS:HE2	2.17	0.60
1:F:39:LEU:HD11	1:F:93:GLY:HA3	1.82	0.60
1:D:100:ASP:CG	1:D:101:ALA:H	2.04	0.60
1:C:100:ASP:OD1	1:C:100:ASP:N	2.32	0.60
2:Q:410:HIS:HA	2:Q:411:LYS:HZ1	1.66	0.60
1:D:19:ILE:O	2:P:426:VAL:HG21	2.01	0.60
1:D:3:GLU:OE1	1:D:3:GLU:HA	2.01	0.60
1:A:143:LEU:HD23	1:A:143:LEU:C	2.22	0.60
1:B:176:GLU:OE2	1:B:179:GLY:C	2.39	0.60
2:N:447:TYR:OH	5:N:550:PHB:H5	2.03	0.59
2:O:473:LYS:HD2	2:O:474:LEU:N	2.18	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:163:GLN:HB3	1:E:165:GLN:NE2	2.18	0.59
1:F:26:ALA:O	2:R:411:LYS:CE	2.50	0.59
1:F:147:ASP:OD2	1:F:174:ARG:HD2	2.02	0.59
2:Q:497:ASN:HD21	2:Q:499:GLU:HB2	1.68	0.59
2:Q:315:TRP:HZ2	2:Q:503:GLN:NE2	2.01	0.59
2:N:497:ASN:HD21	2:N:499:GLU:HB2	1.68	0.59
1:C:52:LEU:CD2	1:C:184:ARG:NH1	2.67	0.58
1:A:65:ASP:OD2	1:A:133:ARG:HD3	2.03	0.58
1:F:78:GLU:CG	2:R:301:PRO:HG2	2.32	0.58
2:R:411:LYS:H	2:R:411:LYS:NZ	2.01	0.58
2:P:361:HIS:HD2	2:P:361:HIS:H	1.51	0.58
2:M:497:ASN:HD22	2:M:499:GLU:N	1.95	0.58
1:C:176:GLU:HG3	1:C:180:LYS:O	2.04	0.58
1:F:18:HIS:CE1	1:F:99:PHE:CE1	2.92	0.58
1:A:165:GLN:H	1:A:165:GLN:NE2	2.02	0.57
1:F:41:LYS:HD2	1:F:88:ALA:HA	1.86	0.57
2:R:376:GLU:OE1	6:R:782:HOH:O	2.17	0.57
1:C:64:ARG:HG2	1:C:64:ARG:NH1	2.19	0.57
1:D:153:ALA:CB	1:D:154:LYS:HE3	2.34	0.57
1:B:176:GLU:HG2	1:B:179:GLY:HA2	1.87	0.57
2:R:356:PHE:CD2	2:R:428:ARG:HD3	2.40	0.57
1:E:67:PHE:CZ	1:E:94:ARG:HD2	2.38	0.57
2:O:363:LEU:HD23	2:O:425:GLY:HA2	1.86	0.57
2:O:364:LEU:HD22	2:O:440:ARG:HD3	1.87	0.56
1:B:131:PHE:CD2	1:B:138:HIS:HB3	2.41	0.56
1:D:168:GLU:HA	1:D:171:ILE:HD12	1.87	0.56
2:R:497:ASN:ND2	2:R:499:GLU:HB2	2.21	0.56
1:C:64:ARG:HG2	1:C:64:ARG:HH11	1.71	0.56
2:P:360:ASP:OD2	2:P:428:ARG:HD2	2.06	0.56
2:M:390:LYS:HD2	6:M:644:HOH:O	2.06	0.55
2:Q:522:ARG:NH1	6:Q:686:HOH:O	2.38	0.55
1:F:143:LEU:HD23	1:F:143:LEU:C	2.26	0.55
1:D:26:ALA:O	2:P:411:LYS:NZ	2.40	0.55
1:F:18:HIS:CE1	1:F:99:PHE:HE1	2.24	0.55
2:P:497:ASN:HD22	2:P:499:GLU:H	1.54	0.55
2:O:361:HIS:CD2	6:O:766:HOH:O	2.59	0.55
1:C:177:VAL:O	1:C:180:LYS:HB3	2.07	0.55
2:Q:364:LEU:HD22	2:Q:440:ARG:HD3	1.88	0.55
2:M:364:LEU:HD22	2:M:440:ARG:CD	2.37	0.55
2:Q:410:HIS:HA	2:Q:411:LYS:NZ	2.22	0.54
1:C:161:ILE:HD13	1:C:196:VAL:HG21	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:GLU:HA	1:D:180:LYS:O	2.07	0.54
1:C:163:GLN:HB3	1:C:165:GLN:HE21	1.70	0.54
2:M:356:PHE:CD1	2:M:428:ARG:HD3	2.42	0.54
1:F:100:ASP:N	1:F:100:ASP:OD1	2.36	0.54
1:C:165:GLN:H	1:C:165:GLN:CD	2.11	0.54
2:M:448:PRO:CB	2:P:516:MET:HA	2.37	0.54
2:N:448:PRO:HD3	2:N:456:TRP:CZ3	2.43	0.54
1:E:84:ASN:OD1	1:E:86:GLU:HB2	2.08	0.54
2:R:497:ASN:HD22	2:R:497:ASN:C	2.12	0.54
1:A:176:GLU:HA	1:A:180:LYS:O	2.08	0.54
1:B:165:GLN:N	1:B:165:GLN:HE21	2.06	0.53
1:B:52:LEU:HD21	1:B:184:ARG:NH1	2.23	0.53
1:A:24:GLU:O	1:A:27:GLY:N	2.34	0.53
1:E:39:LEU:CD1	1:E:106:LEU:HD11	2.38	0.53
1:A:176:GLU:HG2	1:A:179:GLY:CA	2.36	0.53
2:Q:413:ASP:C	2:Q:414:ARG:HD2	2.28	0.53
1:E:134:GLY:HA3	2:Q:326:THR:HG22	1.91	0.53
2:R:413:ASP:C	2:R:414:ARG:HD2	2.29	0.53
2:N:416:LEU:C	2:N:416:LEU:HD23	2.29	0.53
2:Q:416:LEU:HD23	2:Q:417:ALA:N	2.24	0.53
2:N:522:ARG:NH1	6:N:770:HOH:O	2.24	0.53
1:A:131:PHE:CD2	1:A:138:HIS:HB3	2.44	0.53
2:O:447:TYR:HB2	2:O:448:PRO:HD2	1.91	0.52
2:O:361:HIS:HD2	6:O:766:HOH:O	1.93	0.52
1:F:174:ARG:HD2	1:F:183:TYR:OH	2.09	0.52
1:E:39:LEU:HD11	1:E:106:LEU:HD11	1.92	0.52
1:B:52:LEU:HD22	1:B:52:LEU:C	2.30	0.52
2:M:390:LYS:HD3	6:M:720:HOH:O	2.09	0.52
2:R:416:LEU:HD23	2:R:416:LEU:C	2.30	0.52
2:N:414:ARG:NE	2:N:414:ARG:HA	2.25	0.52
1:C:52:LEU:HD21	1:C:184:ARG:NH1	2.24	0.52
1:A:134:GLY:HA3	2:M:326:THR:HG22	1.91	0.52
2:R:360:ASP:OD2	2:R:428:ARG:HD2	2.10	0.52
1:B:165:GLN:CD	1:B:165:GLN:H	2.11	0.52
1:C:100:ASP:CG	1:C:101:ALA:N	2.61	0.51
1:F:50:LEU:C	1:F:50:LEU:HD12	2.31	0.51
2:M:360:ASP:OD2	2:M:428:ARG:HD2	2.10	0.51
2:R:399:MET:HA	2:R:462:HIS:O	2.10	0.51
2:R:534:HIS:HB2	2:R:535:PHE:CD1	2.45	0.51
2:M:364:LEU:HB2	2:M:440:ARG:HD3	1.91	0.51
2:Q:364:LEU:HD22	2:Q:440:ARG:CD	2.40	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:376:GLU:O	2:N:442:ILE:HA	2.10	0.51
1:C:114:VAL:HG23	1:C:122:MET:CE	2.40	0.51
2:M:376:GLU:HG2	2:P:446:PRO:HD2	1.91	0.51
1:A:163:GLN:HB3	1:A:165:GLN:HE21	1.74	0.51
1:F:78:GLU:HB3	1:F:80:GLN:NE2	2.26	0.51
2:N:362:ASP:OD1	2:N:440:ARG:HD3	2.11	0.51
1:B:123:ALA:HB3	1:B:144:TYR:CE1	2.46	0.51
1:C:98:THR:OG1	1:C:101:ALA:HB3	2.11	0.51
2:Q:443:LYS:HE2	6:Q:714:HOH:O	2.11	0.51
2:Q:390:LYS:HD3	6:Q:743:HOH:O	2.10	0.51
1:F:56:TYR:CE1	1:F:62:LEU:HD23	2.46	0.50
2:R:306:SER:CB	2:R:530:GLN:HE21	2.24	0.50
1:D:131:PHE:CD2	1:D:138:HIS:HB3	2.47	0.50
1:A:18:HIS:CE1	1:A:99:PHE:CE1	2.99	0.50
1:B:98:THR:O	1:B:102:GLY:HA2	2.11	0.50
1:D:64:ARG:CG	1:D:64:ARG:HH11	2.12	0.50
1:A:180:LYS:HG2	1:A:181:THR:N	2.27	0.50
2:R:364:LEU:HD22	2:R:440:ARG:HD3	1.92	0.50
1:F:174:ARG:HD2	1:F:183:TYR:CZ	2.47	0.50
2:O:376:GLU:O	2:O:442:ILE:HA	2.10	0.50
1:E:20:GLY:HA2	2:Q:426:VAL:HG13	1.94	0.50
2:P:360:ASP:HB3	2:P:428:ARG:HG3	1.93	0.49
1:F:18:HIS:HD1	1:F:99:PHE:HZ	1.59	0.49
2:Q:364:LEU:HB2	2:Q:440:ARG:HD3	1.93	0.49
1:C:35:ILE:HG21	1:C:92:PHE:HE2	1.77	0.49
2:P:478:LEU:C	2:P:478:LEU:HD23	2.33	0.49
1:F:80:GLN:O	1:F:91:SER:HB2	2.13	0.49
1:F:50:LEU:HB2	1:F:180:LYS:HE2	1.94	0.49
1:B:131:PHE:CE2	1:B:138:HIS:HB3	2.48	0.49
1:A:52:LEU:HD22	1:A:52:LEU:C	2.33	0.49
2:M:416:LEU:C	2:M:416:LEU:HD23	2.33	0.49
1:B:3:GLU:OE1	1:B:3:GLU:HA	2.11	0.48
2:Q:413:ASP:O	2:Q:414:ARG:NH1	2.46	0.48
1:D:18:HIS:HD1	1:D:99:PHE:HZ	1.59	0.48
1:F:147:ASP:OD2	1:F:174:ARG:NH1	2.47	0.48
1:B:114:VAL:HG23	1:B:122:MET:CE	2.44	0.48
2:M:447:TYR:HB2	2:M:448:PRO:HD2	1.95	0.48
2:N:447:TYR:CE1	2:N:460:HIS:HE1	2.31	0.48
2:R:361:HIS:N	2:R:361:HIS:CD2	2.67	0.48
2:O:416:LEU:C	2:O:416:LEU:HD23	2.33	0.48
1:F:100:ASP:CG	1:F:101:ALA:N	2.64	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:98:THR:HG1	1:C:101:ALA:HB3	1.79	0.48
2:R:497:ASN:HD21	2:R:499:GLU:HB2	1.77	0.48
1:E:15:PRO:HB3	1:E:133:ARG:HD2	1.96	0.48
2:R:505:ILE:HG22	2:R:507:LYS:CE	2.43	0.48
2:P:497:ASN:HA	2:P:498:PRO:HD2	1.74	0.48
2:O:411:LYS:HE2	2:O:411:LYS:N	2.23	0.48
2:N:478:LEU:C	2:N:478:LEU:HD23	2.34	0.48
1:F:51:LEU:HD12	1:F:106:LEU:HD23	1.94	0.47
2:M:307:ARG:HG2	2:M:533:THR:HG22	1.96	0.47
2:O:364:LEU:HD22	2:O:440:ARG:CD	2.44	0.47
2:P:356:PHE:HD1	2:P:428:ARG:HD3	1.80	0.47
1:F:35:ILE:HG22	1:F:94:ARG:HG3	1.96	0.47
2:P:313:ARG:O	2:P:318:LYS:CE	2.61	0.47
1:D:24:GLU:O	1:D:27:GLY:CA	2.62	0.47
2:O:356:PHE:HD2	2:O:428:ARG:HD2	1.79	0.47
2:P:390:LYS:HD2	6:P:681:HOH:O	2.13	0.47
1:F:8:THR:HA	1:F:9:PRO:HD3	1.76	0.47
1:A:44:ALA:O	1:A:48:HIS:NE2	2.42	0.47
2:Q:306:SER:HG	2:Q:530:GLN:HE21	1.56	0.47
2:R:410:HIS:HA	2:R:411:LYS:HZ1	1.79	0.47
1:D:28:ASN:HB3	1:D:29:PRO:HD2	1.95	0.47
1:E:18:HIS:CE1	6:E:843:HOH:O	2.67	0.47
2:Q:361:HIS:N	2:Q:361:HIS:CD2	2.66	0.47
2:O:356:PHE:CD2	2:O:428:ARG:HD3	2.50	0.47
1:B:51:LEU:HD11	1:B:126:ILE:CD1	2.45	0.47
2:P:410:HIS:HA	2:P:411:LYS:NZ	2.30	0.47
2:M:497:ASN:ND2	2:M:499:GLU:HB2	2.30	0.47
1:F:147:ASP:OD2	1:F:183:TYR:OH	2.32	0.47
1:E:176:GLU:HA	1:E:180:LYS:O	2.14	0.47
1:A:133:ARG:HG3	2:M:326:THR:HG21	1.96	0.47
1:A:50:LEU:O	1:A:182:ALA:HA	2.15	0.47
1:D:39:LEU:HD13	1:D:106:LEU:HD21	1.97	0.47
1:E:41:LYS:HD2	1:E:87:ASN:O	2.14	0.47
2:R:408:TYR:HE1	2:R:447:TYR:CZ	2.33	0.47
2:R:410:HIS:HA	2:R:411:LYS:HZ3	1.79	0.47
1:F:147:ASP:OD2	1:F:174:ARG:CD	2.63	0.47
2:O:361:HIS:HD2	2:O:361:HIS:H	1.59	0.47
2:Q:392:VAL:HG12	2:Q:395:THR:HB	1.96	0.47
1:A:163:GLN:HA	1:A:164:PRO:HD2	1.81	0.47
2:Q:411:LYS:N	2:Q:411:LYS:CE	2.69	0.47
1:E:100:ASP:CG	1:E:101:ALA:H	2.19	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:489:CYS:HA	2:R:490:PRO:HD3	1.75	0.47
1:E:131:PHE:CD2	1:E:138:HIS:HB3	2.49	0.47
1:E:98:THR:HG1	1:E:103:GLU:H	1.62	0.46
2:N:414:ARG:HD2	2:N:414:ARG:N	2.29	0.46
1:C:50:LEU:O	1:C:182:ALA:HA	2.15	0.46
1:C:65:ASP:OD2	1:C:133:ARG:HD3	2.15	0.46
1:F:18:HIS:HE1	1:F:99:PHE:HE1	1.62	0.46
1:A:163:GLN:CB	1:A:165:GLN:HE22	2.25	0.46
1:F:176:GLU:CG	1:F:179:GLY:HA2	2.43	0.46
2:O:356:PHE:HD2	2:O:428:ARG:CD	2.28	0.46
1:E:184:ARG:HG3	1:E:184:ARG:NH1	2.30	0.46
2:R:411:LYS:HB2	2:R:411:LYS:HE2	1.62	0.46
2:R:447:TYR:OH	5:R:550:PHB:H5	2.15	0.46
2:P:359:HIS:O	2:P:366:ASN:HB3	2.16	0.46
2:Q:411:LYS:HE2	2:Q:411:LYS:HB2	1.69	0.46
1:B:61:HIS:ND1	1:C:163:GLN:HG3	2.31	0.46
2:R:505:ILE:O	2:R:507:LYS:HE3	2.15	0.46
1:C:18:HIS:CE1	6:C:843:HOH:O	2.69	0.46
2:R:405:GLY:HA3	6:R:792:HOH:O	2.13	0.46
2:Q:453:PRO:HB2	2:R:310:ILE:HD12	1.98	0.46
2:Q:408:TYR:HE1	2:Q:447:TYR:CZ	2.33	0.46
2:O:399:MET:HA	2:O:462:HIS:O	2.16	0.46
2:Q:315:TRP:CZ2	2:Q:503:GLN:NE2	2.83	0.46
1:B:39:LEU:HD11	1:B:93:GLY:HA3	1.97	0.46
2:Q:495:ILE:HG21	2:Q:500:ALA:HB3	1.98	0.46
2:Q:376:GLU:O	2:Q:442:ILE:HA	2.15	0.46
1:B:177:VAL:O	1:B:180:LYS:HB3	2.16	0.45
2:M:446:PRO:HD2	2:P:376:GLU:HG2	1.99	0.45
2:M:377:ARG:CZ	2:P:416:LEU:HD21	2.46	0.45
2:O:489:CYS:HA	2:O:490:PRO:HD3	1.74	0.45
1:E:163:GLN:HB3	1:E:165:GLN:HE22	1.80	0.45
2:R:326:THR:HG22	2:R:330:ARG:HD2	1.99	0.45
2:M:335:ALA:HB2	2:O:328:ILE:HD12	1.99	0.45
2:Q:497:ASN:HD22	2:Q:497:ASN:C	2.20	0.45
1:C:114:VAL:HG23	1:C:122:MET:HE2	1.98	0.45
2:Q:316:HIS:HB3	2:Q:317:PRO:HD2	1.97	0.45
1:D:78:GLU:HG2	2:P:301:PRO:CG	2.47	0.45
2:R:315:TRP:HZ2	2:R:503:GLN:NE2	2.11	0.45
1:B:19:ILE:HG22	1:B:26:ALA:HB1	1.99	0.45
2:R:390:LYS:HA	2:R:391:PRO:HD3	1.85	0.45
1:F:24:GLU:O	1:F:27:GLY:CA	2.65	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:176:GLU:HG3	1:B:180:LYS:C	2.37	0.45
2:N:415:TYR:CE1	2:N:416:LEU:HD22	2.52	0.45
1:A:52:LEU:CD2	1:A:184:ARG:NH1	2.80	0.45
1:E:131:PHE:CE2	1:E:138:HIS:HB3	2.51	0.45
1:A:4:LEU:HB3	2:M:387:GLN:HB3	1.98	0.45
1:D:188:ARG:HH11	1:D:188:ARG:HG3	1.81	0.45
2:N:486:ILE:HB	2:N:487:PRO:HD3	1.98	0.45
1:B:64:ARG:HD3	1:B:99:PHE:O	2.17	0.45
1:D:163:GLN:HB3	1:D:165:GLN:NE2	2.32	0.45
1:F:122:MET:HE3	1:F:122:MET:HB2	1.74	0.45
2:Q:400:TRP:HA	2:Q:425:GLY:O	2.16	0.45
2:R:400:TRP:HA	2:R:425:GLY:O	2.16	0.45
2:P:497:ASN:ND2	2:P:499:GLU:HB2	2.31	0.45
2:R:362:ASP:OD1	2:R:440:ARG:HD2	2.17	0.45
2:O:410:HIS:HA	2:O:411:LYS:HZ1	1.82	0.44
1:C:64:ARG:HH11	1:C:64:ARG:CG	2.27	0.44
2:N:497:ASN:HD22	2:N:499:GLU:N	2.04	0.44
2:O:497:ASN:HD22	2:O:499:GLU:H	1.64	0.44
2:O:497:ASN:ND2	2:O:499:GLU:H	2.15	0.44
2:P:410:HIS:HA	2:P:411:LYS:CE	2.47	0.44
2:N:497:ASN:HA	2:N:498:PRO:HD2	1.89	0.44
2:Q:420:ASP:HA	2:Q:421:PRO:HD2	1.88	0.44
2:M:413:ASP:O	2:M:414:ARG:NH1	2.51	0.44
2:M:400:TRP:HA	2:M:425:GLY:O	2.18	0.44
1:D:134:GLY:HA3	2:P:326:THR:HG22	1.99	0.44
2:N:359:HIS:O	2:N:366:ASN:HB3	2.17	0.44
1:C:26:ALA:O	2:O:411:LYS:HE3	2.15	0.44
2:O:414:ARG:N	2:O:414:ARG:HD2	2.32	0.44
2:R:473:LYS:HD2	2:R:474:LEU:N	2.33	0.44
2:M:362:ASP:OD1	2:M:440:ARG:HD2	2.18	0.44
2:Q:414:ARG:N	2:Q:414:ARG:HD2	2.32	0.44
1:D:18:HIS:CE1	1:D:99:PHE:CE1	3.06	0.44
1:D:64:ARG:CG	1:D:64:ARG:NH1	2.64	0.44
1:F:35:ILE:HG21	1:F:92:PHE:HE2	1.82	0.44
2:P:410:HIS:HA	2:P:411:LYS:HZ1	1.83	0.43
1:B:176:GLU:HG3	1:B:180:LYS:N	2.33	0.43
1:C:131:PHE:CD2	1:C:138:HIS:HB3	2.52	0.43
2:P:318:LYS:HD3	2:P:318:LYS:HA	1.57	0.43
1:A:176:GLU:OE2	1:A:179:GLY:HA2	2.18	0.43
1:F:176:GLU:HA	1:F:180:LYS:O	2.18	0.43
2:Q:497:ASN:HA	2:Q:498:PRO:HD2	1.64	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:416:LEU:HD23	2:N:417:ALA:N	2.33	0.43
2:N:413:ASP:C	2:N:414:ARG:HD2	2.39	0.43
1:E:176:GLU:HG3	1:E:180:LYS:C	2.38	0.43
1:B:144:TYR:CE2	1:B:158:LEU:HD13	2.53	0.43
2:O:393:PRO:HG2	2:O:393:PRO:O	2.18	0.43
1:D:24:GLU:O	1:D:27:GLY:HA2	2.18	0.43
1:B:180:LYS:HD2	1:B:181:THR:N	2.33	0.43
2:O:356:PHE:CE2	2:O:428:ARG:HD3	2.54	0.43
1:D:35:ILE:HG21	1:D:92:PHE:HE2	1.84	0.43
2:R:314:ASN:OD1	2:R:318:LYS:HE2	2.19	0.43
2:N:489:CYS:HA	2:N:490:PRO:HD3	1.80	0.43
1:D:25:ALA:C	1:D:27:GLY:N	2.71	0.43
2:R:497:ASN:HD22	2:R:498:PRO:N	2.16	0.43
2:M:362:ASP:CG	2:M:440:ARG:HD2	2.39	0.43
1:F:165:GLN:NE2	1:F:165:GLN:N	2.62	0.43
1:C:54:GLN:HG3	1:C:184:ARG:HH22	1.79	0.43
1:F:176:GLU:HG3	1:F:180:LYS:N	2.34	0.43
2:P:400:TRP:HA	2:P:425:GLY:O	2.18	0.43
2:N:373:PRO:HB3	2:N:423:PHE:HB2	2.01	0.43
2:Q:399:MET:HA	2:Q:462:HIS:O	2.19	0.43
2:R:356:PHE:HD2	2:R:428:ARG:HD3	1.81	0.43
2:R:411:LYS:CD	2:R:411:LYS:H	2.30	0.42
2:P:416:LEU:HD23	2:P:416:LEU:C	2.38	0.42
1:B:176:GLU:HG2	1:B:179:GLY:CA	2.49	0.42
1:A:18:HIS:CE1	1:A:99:PHE:HE1	2.36	0.42
1:B:50:LEU:HD11	1:B:105:THR:HB	2.01	0.42
2:R:416:LEU:HD23	2:R:417:ALA:N	2.34	0.42
1:F:67:PHE:CZ	1:F:94:ARG:HD2	2.55	0.42
1:C:28:ASN:HB3	1:C:29:PRO:HD2	2.01	0.42
1:E:19:ILE:HG21	1:E:19:ILE:HD13	1.68	0.42
2:O:478:LEU:HD12	2:O:523:PHE:CD2	2.54	0.42
1:E:188:ARG:HG3	1:E:188:ARG:HH11	1.84	0.42
1:E:68:LEU:N	1:E:68:LEU:HD12	2.34	0.42
1:A:163:GLN:HG3	1:C:61:HIS:ND1	2.35	0.42
1:D:25:ALA:C	1:D:27:GLY:H	2.22	0.42
1:D:150:GLN:O	1:D:154:LYS:HG2	2.20	0.42
1:E:92:PHE:CD1	2:Q:349:PRO:HG3	2.54	0.42
1:D:164:PRO:O	1:D:167:ARG:HB2	2.19	0.42
1:F:50:LEU:CB	1:F:180:LYS:HE2	2.50	0.42
2:M:372:LEU:HA	2:M:373:PRO:HD3	1.94	0.42
2:M:328:ILE:HD12	2:N:335:ALA:HB2	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:GLN:HA	1:C:164:PRO:HD3	1.88	0.42
1:C:35:ILE:HG21	1:C:92:PHE:CE2	2.54	0.42
2:Q:447:TYR:CE2	2:Q:460:HIS:CE1	3.08	0.42
1:F:131:PHE:O	1:F:132:ALA:HB2	2.20	0.42
1:C:19:ILE:HG21	1:C:19:ILE:HD13	1.81	0.42
2:R:363:LEU:HD23	2:R:425:GLY:HA2	2.01	0.42
1:D:35:ILE:HG21	1:D:92:PHE:CE2	2.55	0.42
2:Q:488:MET:CE	1:F:1:PRO:HG2	2.49	0.42
1:E:5:LEU:HA	1:E:6:PRO:HD3	1.86	0.42
2:O:497:ASN:HD22	2:O:497:ASN:C	2.22	0.42
1:D:191:GLY:O	1:D:194:GLU:HB2	2.19	0.42
1:E:31:ARG:NH1	2:Q:428:ARG:HG2	2.34	0.42
2:R:415:TYR:CE1	2:R:416:LEU:HD22	2.55	0.42
2:O:420:ASP:HA	2:O:421:PRO:HD2	1.81	0.42
1:A:155:CYS:HB3	1:A:158:LEU:HB2	2.02	0.42
2:P:434:ASP:HB3	2:P:436:TYR:CD2	2.55	0.41
2:R:372:LEU:HA	2:R:373:PRO:HD3	1.88	0.41
1:A:100:ASP:N	1:A:100:ASP:OD1	2.41	0.41
2:R:360:ASP:HB3	2:R:428:ARG:HG3	2.02	0.41
1:D:51:LEU:O	1:D:105:THR:HA	2.20	0.41
1:E:100:ASP:N	1:E:100:ASP:OD1	2.45	0.41
1:F:50:LEU:O	1:F:182:ALA:HA	2.20	0.41
1:E:188:ARG:NH1	1:E:188:ARG:HG3	2.36	0.41
1:D:50:LEU:O	1:D:182:ALA:HA	2.20	0.41
1:D:61:HIS:ND1	1:E:163:GLN:HG3	2.35	0.41
1:B:176:GLU:OE2	1:B:179:GLY:O	2.38	0.41
1:C:131:PHE:O	1:C:132:ALA:HB2	2.21	0.41
1:F:74:ASP:HB2	6:F:690:HOH:O	2.19	0.41
1:B:74:ASP:HB2	6:B:690:HOH:O	2.19	0.41
1:E:33:GLN:HG2	1:E:85:LEU:HD12	2.01	0.41
2:P:434:ASP:HB3	2:P:436:TYR:CE2	2.55	0.41
1:B:155:CYS:O	1:B:159:ASN:ND2	2.49	0.41
1:B:147:ASP:OD2	1:B:183:TYR:OH	2.29	0.41
2:P:360:ASP:HB3	2:P:428:ARG:CG	2.50	0.41
2:O:497:ASN:HA	2:O:498:PRO:HD2	1.82	0.41
2:Q:486:ILE:HB	2:Q:487:PRO:HD3	2.01	0.41
1:E:74:ASP:N	1:E:78:GLU:O	2.50	0.41
1:F:98:THR:O	1:F:102:GLY:HA2	2.21	0.41
1:A:100:ASP:CG	1:A:101:ALA:N	2.73	0.41
2:R:411:LYS:N	2:R:411:LYS:HE2	2.31	0.41
1:B:100:ASP:CG	1:B:101:ALA:H	2.23	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Q:495:ILE:CG2	2:Q:500:ALA:HB3	2.50	0.41
2:M:377:ARG:NE	2:P:416:LEU:HD21	2.35	0.41
2:Q:489:CYS:HA	2:Q:490:PRO:HD3	1.84	0.41
1:E:4:LEU:HB3	2:Q:387:GLN:HB3	2.03	0.41
2:M:497:ASN:HA	2:M:498:PRO:HD2	1.76	0.41
2:N:361:HIS:N	2:N:361:HIS:CD2	2.79	0.41
2:N:383:ARG:HG3	2:N:436:TYR:CZ	2.56	0.41
2:M:362:ASP:OD1	2:M:440:ARG:CD	2.68	0.41
1:C:176:GLU:HG3	1:C:180:LYS:C	2.41	0.41
1:F:158:LEU:HD12	1:F:161:ILE:HD12	2.03	0.41
1:E:61:HIS:CE1	1:F:163:GLN:HG3	2.54	0.41
1:F:25:ALA:C	1:F:27:GLY:H	2.23	0.41
1:A:131:PHE:CD2	2:M:475:ILE:HD12	2.56	0.41
2:P:408:TYR:HE2	2:P:447:TYR:CZ	2.39	0.41
1:E:114:VAL:HG23	1:E:122:MET:CE	2.51	0.41
2:M:488:MET:CE	2:P:508:LEU:HD23	2.51	0.41
2:M:383:ARG:HH11	2:M:383:ARG:HD3	1.57	0.41
1:B:133:ARG:HG3	2:N:326:THR:HG21	2.03	0.40
1:F:113:VAL:HG13	1:F:122:MET:O	2.21	0.40
2:P:447:TYR:HA	2:P:448:PRO:HD3	1.95	0.40
2:P:411:LYS:N	2:P:411:LYS:CE	2.40	0.40
2:M:360:ASP:HB3	2:M:428:ARG:HG3	2.03	0.40
2:O:381:ALA:O	2:O:522:ARG:HA	2.21	0.40
1:E:51:LEU:HD11	1:E:126:ILE:CD1	2.51	0.40
1:C:39:LEU:HD11	1:C:93:GLY:HA3	2.03	0.40
1:A:78:GLU:HG2	2:M:301:PRO:HG3	2.03	0.40
1:C:84:ASN:OD1	1:C:86:GLU:HB2	2.20	0.40
2:O:315:TRP:HZ2	2:O:503:GLN:HE21	1.69	0.40
1:B:100:ASP:N	1:B:100:ASP:OD1	2.46	0.40
2:O:356:PHE:CD2	2:O:428:ARG:CD	3.04	0.40
1:A:28:ASN:HB3	1:A:29:PRO:HD2	2.04	0.40
1:B:123:ALA:HB3	1:B:144:TYR:HE1	1.86	0.40
2:P:326:THR:O	2:P:326:THR:HG22	2.21	0.40
1:D:77:GLY:O	1:D:114:VAL:HG12	2.22	0.40
1:E:66:SER:HB2	1:E:130:LEU:HD11	2.04	0.40
2:P:487:PRO:O	2:P:493:LYS:HD3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	198/200 (99%)	192 (97%)	6 (3%)	0	100	100
1	B	198/200 (99%)	192 (97%)	6 (3%)	0	100	100
1	C	198/200 (99%)	192 (97%)	6 (3%)	0	100	100
1	D	198/200 (99%)	190 (96%)	8 (4%)	0	100	100
1	E	198/200 (99%)	188 (95%)	10 (5%)	0	100	100
1	F	198/200 (99%)	191 (96%)	7 (4%)	0	100	100
2	M	229/238 (96%)	221 (96%)	8 (4%)	0	100	100
2	N	229/238 (96%)	223 (97%)	6 (3%)	0	100	100
2	O	229/238 (96%)	222 (97%)	7 (3%)	0	100	100
2	P	229/238 (96%)	224 (98%)	5 (2%)	0	100	100
2	Q	229/238 (96%)	220 (96%)	9 (4%)	0	100	100
2	R	229/238 (96%)	221 (96%)	8 (4%)	0	100	100
All	All	2562/2628 (98%)	2476 (97%)	86 (3%)	0	100	100

There are no Ramachandran outliers to report.

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 X-ray entries followed by that with respect to entries of similar resolution.

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	162/163 (99%)	155 (96%)	7 (4%)	35	28
1	B	162/163 (99%)	151 (93%)	11 (7%)	20	12

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	162/163 (99%)	156 (96%)	6 (4%)	41	35
1	D	162/163 (99%)	154 (95%)	8 (5%)	31	22
1	E	162/163 (99%)	155 (96%)	7 (4%)	35	28
1	F	162/163 (99%)	153 (94%)	9 (6%)	26	18
2	M	196/202 (97%)	188 (96%)	8 (4%)	37	30
2	N	196/202 (97%)	184 (94%)	12 (6%)	23	15
2	O	196/202 (97%)	187 (95%)	9 (5%)	33	25
2	P	196/202 (97%)	186 (95%)	10 (5%)	29	21
2	Q	196/202 (97%)	185 (94%)	11 (6%)	26	18
2	R	196/202 (97%)	186 (95%)	10 (5%)	29	21
All	All	2148/2190 (98%)	2040 (95%)	108 (5%)	30	22

All (108) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	19	ILE
1	A	38	ARG
1	A	52	LEU
1	A	106	LEU
1	A	133	ARG
1	A	165	GLN
2	M	372	LEU
2	M	395	THR
2	M	416	LEU
2	M	434	ASP
2	M	440	ARG
2	M	497	ASN
2	M	507	LYS
2	M	534	HIS
1	B	4	LEU
1	B	19	ILE
1	B	32	ASP
1	B	38	ARG
1	B	52	LEU
1	B	106	LEU
1	B	141	THR
1	B	150	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	165	GLN
1	B	176	GLU
1	B	184	ARG
2	N	364	LEU
2	N	372	LEU
2	N	395	THR
2	N	399	MET
2	N	411	LYS
2	N	414	ARG
2	N	416	LEU
2	N	433	SER
2	N	440	ARG
2	N	497	ASN
2	N	507	LYS
2	N	534	HIS
1	C	4	LEU
1	C	19	ILE
1	C	38	ARG
1	C	52	LEU
1	C	133	ARG
1	C	165	GLN
2	O	372	LEU
2	O	393	PRO
2	O	395	THR
2	O	411	LYS
2	O	416	LEU
2	O	434	ASP
2	O	473	LYS
2	O	487	PRO
2	O	497	ASN
1	D	4	LEU
1	D	19	ILE
1	D	38	ARG
1	D	42	PRO
1	D	52	LEU
1	D	106	LEU
1	D	133	ARG
1	D	165	GLN
2	P	395	THR
2	P	411	LYS
2	P	414	ARG
2	P	416	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	P	434	ASP
2	P	440	ARG
2	P	488	MET
2	P	497	ASN
2	P	503	GLN
2	P	534	HIS
1	E	4	LEU
1	E	19	ILE
1	E	38	ARG
1	E	52	LEU
1	E	133	ARG
1	E	165	GLN
1	E	180	LYS
2	Q	395	THR
2	Q	399	MET
2	Q	411	LYS
2	Q	416	LEU
2	Q	428	ARG
2	Q	434	ASP
2	Q	440	ARG
2	Q	497	ASN
2	Q	499	GLU
2	Q	507	LYS
2	Q	534	HIS
1	F	4	LEU
1	F	19	ILE
1	F	38	ARG
1	F	50	LEU
1	F	52	LEU
1	F	114	VAL
1	F	165	GLN
1	F	178	ASP
1	F	180	LYS
2	R	372	LEU
2	R	395	THR
2	R	411	LYS
2	R	416	LEU
2	R	428	ARG
2	R	434	ASP
2	R	442	ILE
2	R	478	LEU
2	R	497	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	R	507	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	163	GLN
1	A	165	GLN
2	M	361	HIS
2	M	412	ASN
2	M	497	ASN
2	M	503	GLN
1	B	165	GLN
2	N	361	HIS
2	N	497	ASN
2	N	503	GLN
1	C	163	GLN
1	C	165	GLN
2	O	361	HIS
2	O	412	ASN
2	O	497	ASN
2	O	503	GLN
1	D	163	GLN
1	D	165	GLN
2	P	361	HIS
2	P	412	ASN
2	P	497	ASN
2	P	503	GLN
1	E	165	GLN
2	Q	361	HIS
2	Q	497	ASN
2	Q	503	GLN
2	Q	530	GLN
1	F	80	GLN
1	F	165	GLN
2	R	361	HIS
2	R	422	ASN
2	R	497	ASN
2	R	503	GLN
2	R	530	GLN

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 24 ligands modelled in this entry, 6 are monoatomic - leaving 18 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	$\# Z > 2$
5	PHB	M	550	3	7,10,10	1.08	0	10,13,13	0.84	0
5	PHB	M	551	-	7,10,10	0.62	0	10,13,13	0.44	0
4	BME	M	601	2	3,3,3	0.37	0	2,2,2	0.78	0
5	PHB	N	550	3	7,10,10	0.63	0	10,13,13	0.88	0
5	PHB	N	551	-	7,10,10	0.51	0	10,13,13	0.40	0
4	BME	N	601	2	3,3,3	0.31	0	2,2,2	0.04	0
5	PHB	O	550	3	7,10,10	0.91	0	10,13,13	1.03	0
5	PHB	O	551	-	7,10,10	0.94	0	10,13,13	0.84	0
4	BME	O	601	2	3,3,3	0.75	0	2,2,2	0.71	0
5	PHB	P	550	3	7,10,10	0.79	0	10,13,13	0.87	0
5	PHB	P	551	-	7,10,10	0.88	0	10,13,13	0.80	0
4	BME	P	601	2	3,3,3	0.61	0	2,2,2	1.02	0
5	PHB	Q	550	3	7,10,10	1.02	0	10,13,13	0.95	0
5	PHB	Q	551	-	7,10,10	0.89	0	10,13,13	0.64	0
4	BME	Q	601	2	3,3,3	0.66	0	2,2,2	1.08	0
5	PHB	R	550	3	7,10,10	0.69	0	10,13,13	0.62	0
5	PHB	R	551	-	7,10,10	0.75	0	10,13,13	0.67	0
4	BME	R	601	2	3,3,3	0.34	0	2,2,2	0.26	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PHB	M	550	3	-	0/0/4/4	0/1/1/1
5	PHB	M	551	-	-	0/0/4/4	0/1/1/1
4	BME	M	601	2	-	0/1/1/1	0/0/0/0
5	PHB	N	550	3	-	0/0/4/4	0/1/1/1
5	PHB	N	551	-	-	0/0/4/4	0/1/1/1
4	BME	N	601	2	-	0/1/1/1	0/0/0/0
5	PHB	O	550	3	-	0/0/4/4	0/1/1/1
5	PHB	O	551	-	-	0/0/4/4	0/1/1/1
4	BME	O	601	2	-	0/1/1/1	0/0/0/0
5	PHB	P	550	3	-	0/0/4/4	0/1/1/1
5	PHB	P	551	-	-	0/0/4/4	0/1/1/1
4	BME	P	601	2	-	0/1/1/1	0/0/0/0
5	PHB	Q	550	3	-	0/0/4/4	0/1/1/1
5	PHB	Q	551	-	-	0/0/4/4	0/1/1/1
4	BME	Q	601	2	-	0/1/1/1	0/0/0/0
5	PHB	R	550	3	-	0/0/4/4	0/1/1/1
5	PHB	R	551	-	-	0/0/4/4	0/1/1/1
4	BME	R	601	2	-	0/1/1/1	0/0/0/0

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	N	550	PHB	1	0
5	R	550	PHB	1	0

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.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.