



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 18, 2023 – 02:37 PM EDT

PDB ID : 3PCK
Title : STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COM-
PLEXED WITH 6-HYDROXYNICOTINIC ACID N-OXIDE
Authors : Orville, A.M.; Lipscomb, J.D.; Ohlendorf, D.H.
Deposited on : 1997-07-18
Resolution : 2.13 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

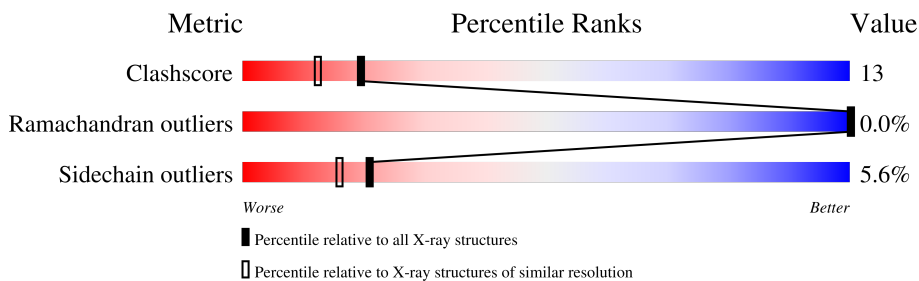
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.13 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	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)





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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	200	70% 26% .
1	B	200	68% 28% .
1	C	200	71% 24% . .
1	D	200	70% 26% 5%
1	E	200	70% 26% .
1	F	200	64% 30% 6%
2	M	238	68% 24% 5% . .
2	N	238	74% 21% . .

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Mol	Chain	Length	Quality of chain
2	O	238	 71% 22% 5% .
2	P	238	 74% 19% . . .
2	Q	238	 71% 21% 5% .
2	R	238	 69% 23% 5% . .

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 22014 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
			Total	C	N	O	S			
1	A	200	1571	993	276	299	3	0	0	0
1	B	200	1571	993	276	299	3	0	0	0
1	C	200	1571	993	276	299	3	0	0	0
1	D	200	1571	993	276	299	3	0	0	0
1	E	200	1571	993	276	299	3	0	0	0
1	F	200	1571	993	276	299	3	0	0	0

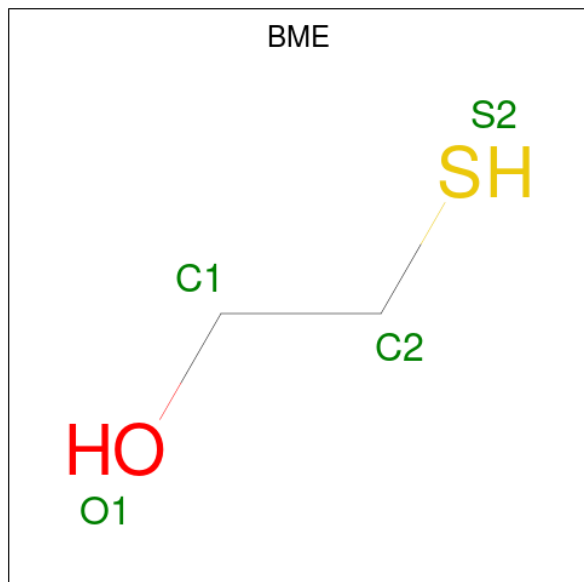
- Molecule 2 is a protein called PROTOCATECHUATE 3,4-DIOXYGENASE.

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

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

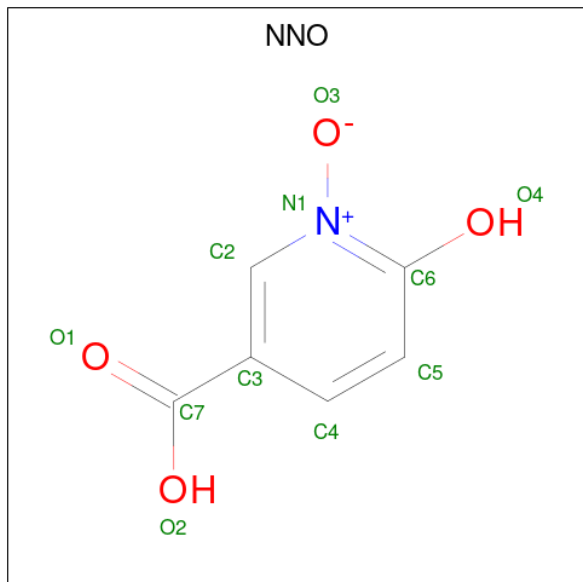
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	M	1	Total Fe 1 1	0	0
3	N	1	Total Fe 1 1	0	0
3	O	1	Total Fe 1 1	0	0
3	P	1	Total Fe 1 1	0	0
3	Q	1	Total Fe 1 1	0	0
3	R	1	Total Fe 1 1	0	0

- Molecule 4 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C₂H₆OS).



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 6-HYDROXYISONICOTINIC ACID N-OXIDE (three-letter code: NNO) (formula: C₆H₅NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	M	1	11	6	1	4	0	0
5	N	1	11	6	1	4	0	0
5	O	1	11	6	1	4	0	0
5	P	1	11	6	1	4	0	0
5	Q	1	11	6	1	4	0	0
5	R	1	11	6	1	4	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	86	86	86	0	0
6	M	155	155	155	0	0
6	B	85	85	85	0	0
6	N	160	160	160	0	0

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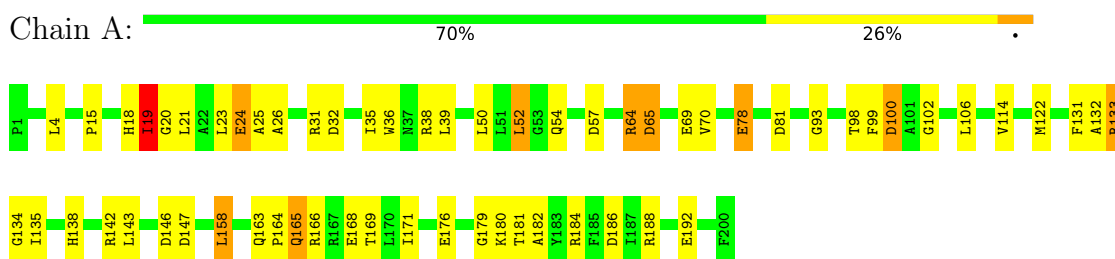
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	83	Total O 83 83	0	0
6	O	157	Total O 157 157	0	0
6	D	81	Total O 81 81	0	0
6	P	155	Total O 155 155	0	0
6	E	86	Total O 86 86	0	0
6	Q	161	Total O 161 161	0	0
6	F	86	Total O 86 86	0	0
6	R	157	Total O 157 157	0	0

3 Residue-property plots

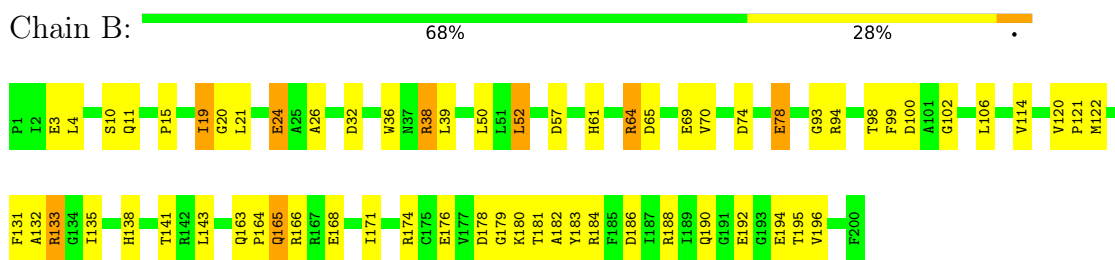
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

Note EDS was not executed.

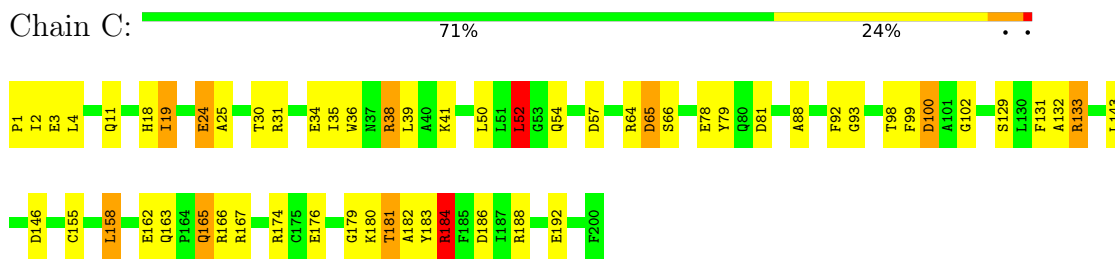
- Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE



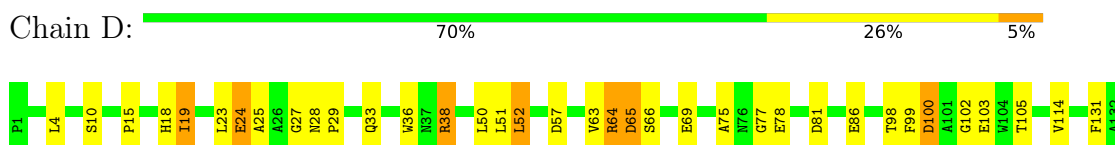
- Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE



- Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE

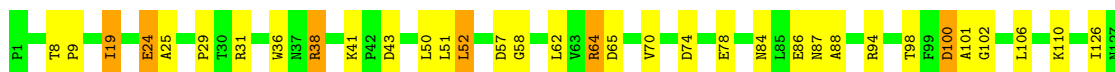


- Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE

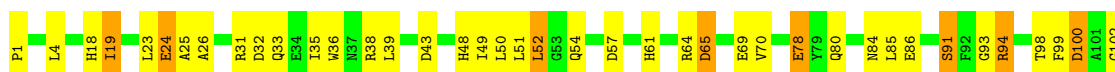




- Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE



- Molecule 1: PROTOCATECHUATE 3,4-DIOXYGENASE



- Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE

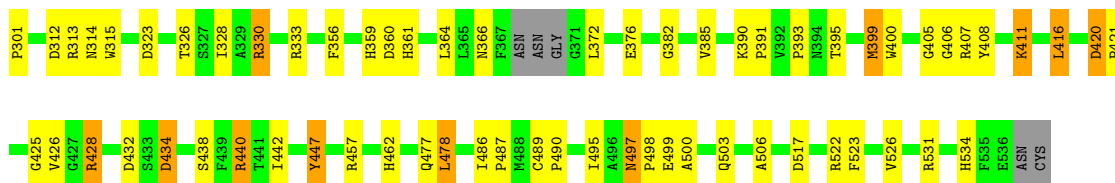


- Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE



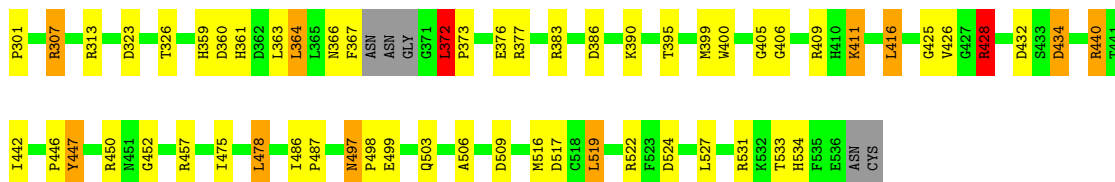
- Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE





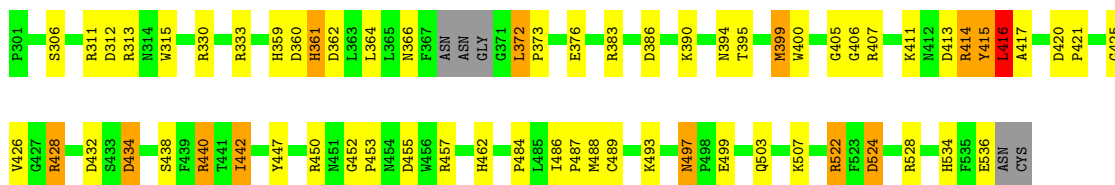
• Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE

Chain P: 74% 19%



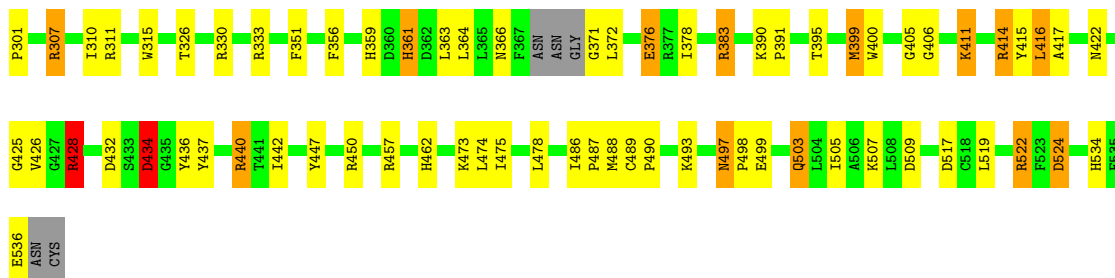
• Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE

Chain Q: 71% 21% 5%



• Molecule 2: PROTOCATECHUATE 3,4-DIOXYGENASE

Chain R: 69% 23% 5%



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	196.90Å 127.80Å 134.40Å 90.00° 97.80° 90.00°	Depositor
Resolution (Å)	6.00 – 2.13	Depositor
% Data completeness (in resolution range)	88.0 (6.00-2.13)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.173 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	22014	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

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: BME, NNO, FE

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	1.00	1/1611 (0.1%)	1.66	30/2195 (1.4%)
1	B	1.01	1/1611 (0.1%)	1.62	27/2195 (1.2%)
1	C	1.00	0/1611	1.49	20/2195 (0.9%)
1	D	1.01	1/1611 (0.1%)	1.55	24/2195 (1.1%)
1	E	0.98	0/1611	1.58	25/2195 (1.1%)
1	F	1.03	0/1611	1.60	20/2195 (0.9%)
2	M	1.11	2/1895 (0.1%)	1.66	32/2580 (1.2%)
2	N	1.08	0/1895	1.69	28/2580 (1.1%)
2	O	1.10	1/1895 (0.1%)	1.64	28/2580 (1.1%)
2	P	1.10	2/1895 (0.1%)	1.65	31/2580 (1.2%)
2	Q	1.12	0/1895	1.66	35/2580 (1.4%)
2	R	1.09	0/1895	1.56	24/2580 (0.9%)
All	All	1.06	8/21036 (0.0%)	1.62	324/28650 (1.1%)

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	C	0	1
2	M	0	1
All	All	0	2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	313	ARG	NE-CZ	6.41	1.41	1.33
2	M	428	ARG	CD-NE	-6.05	1.36	1.46
1	A	133	ARG	CD-NE	-5.73	1.36	1.46
2	M	345	GLU	CD-OE1	-5.71	1.19	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	10	SER	CA-CB	5.53	1.61	1.52
1	D	10	SER	CA-CB	5.31	1.60	1.52
2	P	367	PHE	C-O	5.25	1.33	1.23
2	P	452	GLY	CA-C	5.15	1.60	1.51

All (324) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	440	ARG	NE-CZ-NH2	-21.96	109.32	120.30
2	N	428	ARG	NE-CZ-NH1	19.28	129.94	120.30
2	O	440	ARG	NE-CZ-NH2	-18.40	111.10	120.30
2	P	440	ARG	NE-CZ-NH2	-17.81	111.40	120.30
2	P	457	ARG	NE-CZ-NH1	17.58	129.09	120.30
2	Q	440	ARG	NE-CZ-NH2	-15.86	112.37	120.30
2	M	428	ARG	NE-CZ-NH1	15.57	128.09	120.30
1	B	184	ARG	NE-CZ-NH2	-15.26	112.67	120.30
2	R	440	ARG	NE-CZ-NH2	-15.05	112.78	120.30
2	M	428	ARG	CD-NE-CZ	14.96	144.55	123.60
1	F	38	ARG	NE-CZ-NH1	14.50	127.55	120.30
2	M	440	ARG	NE-CZ-NH2	-14.41	113.09	120.30
2	Q	428	ARG	NE-CZ-NH1	14.29	127.45	120.30
2	O	428	ARG	NE-CZ-NH1	14.25	127.43	120.30
1	A	166	ARG	NE-CZ-NH1	14.02	127.31	120.30
2	O	428	ARG	CD-NE-CZ	13.91	143.07	123.60
1	A	133	ARG	CD-NE-CZ	13.75	142.84	123.60
1	B	184	ARG	NE-CZ-NH1	13.55	127.07	120.30
2	P	440	ARG	NE-CZ-NH1	13.34	126.97	120.30
2	Q	428	ARG	NE-CZ-NH2	-13.14	113.73	120.30
1	A	166	ARG	NE-CZ-NH2	-12.85	113.87	120.30
1	B	133	ARG	NE-CZ-NH2	-12.69	113.95	120.30
2	N	428	ARG	NE-CZ-NH2	-12.43	114.08	120.30
1	F	38	ARG	NE-CZ-NH2	-12.43	114.09	120.30
2	O	333	ARG	NE-CZ-NH2	-12.36	114.12	120.30
2	P	457	ARG	CD-NE-CZ	11.96	140.34	123.60
2	R	522	ARG	NE-CZ-NH1	-11.90	114.35	120.30
1	D	133	ARG	NE-CZ-NH2	-11.69	114.46	120.30
2	N	440	ARG	NE-CZ-NH1	11.68	126.14	120.30
1	B	38	ARG	NE-CZ-NH2	-11.64	114.48	120.30
2	O	428	ARG	NE-CZ-NH2	-11.50	114.55	120.30
1	A	133	ARG	NE-CZ-NH2	-11.48	114.56	120.30
2	Q	428	ARG	CD-NE-CZ	11.43	139.60	123.60
2	M	333	ARG	NE-CZ-NH2	-11.25	114.67	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Q	457	ARG	NE-CZ-NH2	-11.16	114.72	120.30
2	N	457	ARG	NE-CZ-NH2	-11.02	114.79	120.30
2	R	428	ARG	NE-CZ-NH2	-10.93	114.84	120.30
2	N	528	ARG	NE-CZ-NH2	-10.77	114.92	120.30
2	M	428	ARG	NE-CZ-NH2	-10.76	114.92	120.30
2	N	428	ARG	CD-NE-CZ	10.55	138.37	123.60
2	Q	311	ARG	NE-CZ-NH1	10.47	125.53	120.30
1	F	188	ARG	NE-CZ-NH1	10.21	125.41	120.30
2	Q	522	ARG	NE-CZ-NH1	-10.18	115.21	120.30
2	Q	524	ASP	CB-CG-OD2	-9.93	109.36	118.30
2	Q	528	ARG	NE-CZ-NH2	-9.91	115.35	120.30
1	A	188	ARG	NE-CZ-NH1	9.89	125.25	120.30
2	Q	450	ARG	NE-CZ-NH1	9.87	125.23	120.30
1	F	142	ARG	NE-CZ-NH1	9.77	125.19	120.30
2	O	330	ARG	NE-CZ-NH2	-9.61	115.50	120.30
1	F	38	ARG	CD-NE-CZ	9.59	137.02	123.60
1	E	94	ARG	NE-CZ-NH1	9.56	125.08	120.30
2	M	313	ARG	NE-CZ-NH1	9.51	125.06	120.30
2	N	420	ASP	CB-CG-OD2	-9.29	109.93	118.30
2	P	432	ASP	CB-CG-OD1	9.29	126.66	118.30
1	C	188	ARG	NE-CZ-NH1	9.25	124.92	120.30
2	O	517	ASP	CB-CG-OD1	9.18	126.57	118.30
2	M	457	ARG	CD-NE-CZ	9.09	136.32	123.60
2	R	440	ARG	NE-CZ-NH1	9.06	124.83	120.30
1	E	186	ASP	CB-CG-OD1	9.06	126.45	118.30
2	M	313	ARG	NE-CZ-NH2	-8.90	115.85	120.30
2	M	312	ASP	CB-CG-OD2	-8.86	110.33	118.30
1	E	94	ARG	NE-CZ-NH2	-8.73	115.93	120.30
1	F	94	ARG	NE-CZ-NH2	-8.71	115.94	120.30
1	E	133	ARG	NE-CZ-NH2	-8.58	116.01	120.30
2	N	524	ASP	CB-CG-OD2	-8.54	110.62	118.30
1	C	186	ASP	CB-CG-OD1	8.45	125.90	118.30
2	O	457	ARG	NE-CZ-NH1	8.43	124.52	120.30
2	R	428	ARG	NE-CZ-NH1	8.40	124.50	120.30
2	Q	450	ARG	NE-CZ-NH2	-8.37	116.12	120.30
2	R	376	GLU	OE1-CD-OE2	8.31	133.28	123.30
2	P	524	ASP	CB-CG-OD2	-8.27	110.86	118.30
2	R	522	ARG	NE-CZ-NH2	8.27	124.43	120.30
2	M	407	ARG	NE-CZ-NH1	8.24	124.42	120.30
1	B	65	ASP	CB-CG-OD1	8.23	125.71	118.30
1	C	133	ARG	CD-NE-CZ	8.02	134.83	123.60
1	D	133	ARG	NE-CZ-NH1	7.98	124.29	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	186	ASP	CB-CG-OD2	-7.98	111.12	118.30
2	Q	414	ARG	NE-CZ-NH1	7.96	124.28	120.30
2	M	428	ARG	CG-CD-NE	7.95	128.49	111.80
1	D	166	ARG	NE-CZ-NH1	7.92	124.26	120.30
1	A	184	ARG	NE-CZ-NH1	7.87	124.23	120.30
2	Q	312	ASP	CB-CG-OD1	7.79	125.31	118.30
2	P	313	ARG	NE-CZ-NH1	7.77	124.19	120.30
1	E	38	ARG	CD-NE-CZ	-7.77	112.72	123.60
2	N	333	ARG	NE-CZ-NH2	-7.77	116.42	120.30
1	C	133	ARG	NE-CZ-NH2	-7.73	116.44	120.30
2	Q	440	ARG	NE-CZ-NH1	7.65	124.12	120.30
1	D	184	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	F	142	ARG	NE-CZ-NH2	-7.53	116.54	120.30
2	M	432	ASP	CB-CG-OD2	-7.49	111.56	118.30
2	M	528	ARG	NE-CZ-NH2	-7.44	116.58	120.30
1	A	133	ARG	NE-CZ-NH1	7.44	124.02	120.30
1	A	142	ARG	CD-NE-CZ	7.38	133.93	123.60
2	Q	330	ARG	NE-CZ-NH1	7.36	123.98	120.30
2	P	457	ARG	NE-CZ-NH2	-7.31	116.65	120.30
1	C	133	ARG	NE-CZ-NH1	7.29	123.94	120.30
1	D	57	ASP	CB-CG-OD1	7.27	124.84	118.30
1	D	75	ALA	CB-CA-C	7.26	121.00	110.10
1	D	167	ARG	NE-CZ-NH1	7.26	123.93	120.30
1	A	36	TRP	CB-CA-C	7.25	124.89	110.40
2	P	509	ASP	CB-CG-OD2	-7.24	111.78	118.30
2	P	524	ASP	CB-CG-OD1	7.23	124.81	118.30
2	O	457	ARG	CD-NE-CZ	7.17	133.64	123.60
2	O	457	ARG	NE-CZ-NH2	-7.17	116.72	120.30
1	F	57	ASP	CB-CG-OD2	-7.15	111.87	118.30
1	E	74	ASP	CB-CG-OD2	-7.13	111.88	118.30
1	B	166	ARG	NE-CZ-NH2	-7.01	116.79	120.30
2	P	377	ARG	NE-CZ-NH1	-7.01	116.80	120.30
2	O	407	ARG	NE-CZ-NH2	-7.01	116.80	120.30
2	R	522	ARG	CD-NE-CZ	-7.01	113.79	123.60
2	R	457	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	A	146	ASP	CB-CG-OD1	6.98	124.58	118.30
2	O	440	ARG	NH1-CZ-NH2	6.94	127.03	119.40
2	R	517	ASP	CB-CG-OD1	6.93	124.54	118.30
2	M	434	ASP	CB-CG-OD2	-6.92	112.07	118.30
2	Q	434	ASP	CB-CG-OD2	-6.90	112.09	118.30
2	M	517	ASP	CB-CG-OD2	-6.89	112.10	118.30
1	D	57	ASP	CB-CG-OD2	-6.88	112.11	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	133	ARG	NE-CZ-NH1	6.86	123.73	120.30
2	P	434	ASP	CB-CG-OD2	-6.85	112.14	118.30
1	E	174	ARG	NE-CZ-NH1	6.84	123.72	120.30
1	B	32	ASP	CB-CG-OD1	6.83	124.44	118.30
2	P	447	TYR	CB-CG-CD2	6.81	125.09	121.00
1	A	184	ARG	CD-NE-CZ	6.80	133.13	123.60
2	Q	428	ARG	CG-CD-NE	6.78	126.04	111.80
1	E	52	LEU	CB-CA-C	6.77	123.07	110.20
1	D	65	ASP	CB-CG-OD1	6.73	124.36	118.30
2	P	409	ARG	NE-CZ-NH1	6.73	123.67	120.30
2	M	524	ASP	CB-CG-OD1	6.69	124.32	118.30
1	A	52	LEU	CB-CA-C	6.68	122.90	110.20
1	A	184	ARG	NE-CZ-NH2	-6.68	116.96	120.30
1	C	65	ASP	CB-CG-OD1	6.68	124.31	118.30
1	C	38	ARG	CD-NE-CZ	-6.67	114.26	123.60
2	O	330	ARG	NE-CZ-NH1	6.67	123.63	120.30
2	Q	313	ARG	CD-NE-CZ	6.66	132.92	123.60
2	N	428	ARG	CG-CD-NE	6.63	125.73	111.80
2	R	376	GLU	CG-CD-OE2	-6.62	105.07	118.30
2	R	434	ASP	CB-CG-OD1	-6.59	112.37	118.30
2	R	311	ARG	NE-CZ-NH2	-6.56	117.02	120.30
1	B	188	ARG	NE-CZ-NH1	6.54	123.57	120.30
1	F	38	ARG	CA-CB-CG	6.53	127.77	113.40
2	N	313	ARG	NE-CZ-NH1	6.46	123.53	120.30
2	Q	524	ASP	CB-CG-OD1	6.46	124.11	118.30
2	Q	432	ASP	CB-CG-OD1	6.44	124.09	118.30
2	N	457	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	F	36	TRP	CB-CA-C	6.36	123.12	110.40
2	O	434	ASP	CB-CG-OD2	-6.34	112.60	118.30
2	P	432	ASP	CB-CG-OD2	-6.33	112.60	118.30
2	R	457	ARG	CA-CB-CG	6.33	127.33	113.40
1	E	166	ARG	NE-CZ-NH1	6.33	123.46	120.30
1	B	186	ASP	CB-CG-OD1	6.30	123.97	118.30
2	N	509	ASP	CB-CG-OD1	6.29	123.97	118.30
1	F	65	ASP	CB-CG-OD1	6.29	123.96	118.30
2	M	440	ARG	NE-CZ-NH1	6.27	123.44	120.30
1	B	36	TRP	CB-CA-C	6.26	122.92	110.40
1	E	57	ASP	CB-CG-OD2	-6.26	112.67	118.30
1	D	23	LEU	CB-CA-C	6.25	122.07	110.20
2	O	428	ARG	CG-CD-NE	6.22	124.87	111.80
2	M	307	ARG	NE-CZ-NH1	6.21	123.40	120.30
1	F	133	ARG	CA-CB-CG	6.17	126.98	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	ARG	NE-CZ-NH2	-6.16	117.22	120.30
1	E	188	ARG	NE-CZ-NH1	6.13	123.36	120.30
1	E	36	TRP	CB-CA-C	6.12	122.64	110.40
2	O	506	ALA	N-CA-CB	6.11	118.66	110.10
2	Q	312	ASP	CB-CG-OD2	-6.11	112.80	118.30
2	Q	333	ARG	NE-CZ-NH2	-6.11	117.25	120.30
1	A	188	ARG	NE-CZ-NH2	-6.08	117.26	120.30
2	O	531	ARG	NE-CZ-NH1	6.08	123.34	120.30
1	A	57	ASP	CB-CG-OD1	6.05	123.75	118.30
1	B	178	ASP	CB-CG-OD1	6.05	123.75	118.30
1	B	188	ARG	NE-CZ-NH2	-6.05	117.28	120.30
2	P	416	LEU	CA-CB-CG	6.03	129.16	115.30
1	D	64	ARG	NE-CZ-NH1	6.01	123.31	120.30
1	E	146	ASP	CB-CG-OD1	6.01	123.71	118.30
2	M	457	ARG	CG-CD-NE	6.00	124.41	111.80
2	N	450	ARG	NE-CZ-NH1	6.00	123.30	120.30
2	R	509	ASP	CB-CG-OD1	5.98	123.68	118.30
1	A	32	ASP	CB-CG-OD1	5.96	123.66	118.30
1	C	183	TYR	N-CA-CB	5.95	121.31	110.60
1	E	31	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	A	186	ASP	CB-CG-OD1	5.92	123.62	118.30
1	D	36	TRP	CB-CA-C	5.92	122.23	110.40
1	F	166	ARG	NE-CZ-NH1	5.91	123.25	120.30
1	F	146	ASP	CB-CG-OD2	-5.90	112.99	118.30
2	M	376	GLU	OE1-CD-OE2	5.90	130.38	123.30
1	F	52	LEU	CB-CA-C	5.90	121.42	110.20
2	O	432	ASP	CB-CG-OD2	-5.89	113.00	118.30
1	C	52	LEU	CB-CA-C	5.89	121.39	110.20
1	A	81	ASP	CB-CG-OD1	5.87	123.59	118.30
1	D	146	ASP	CB-CG-OD1	5.86	123.58	118.30
2	M	323	ASP	CB-CG-OD2	-5.85	113.04	118.30
1	B	52	LEU	CB-CA-C	5.83	121.28	110.20
2	M	312	ASP	CB-CG-OD1	5.82	123.54	118.30
2	Q	383	ARG	CD-NE-CZ	-5.82	115.45	123.60
2	P	428	ARG	NE-CZ-NH1	5.82	123.21	120.30
2	O	420	ASP	CB-CG-OD1	5.80	123.52	118.30
2	M	447	TYR	N-CA-CB	-5.78	100.20	110.60
1	C	129	SER	N-CA-CB	5.78	119.16	110.50
1	D	166	ARG	NE-CZ-NH2	-5.78	117.41	120.30
1	B	11	GLN	N-CA-CB	5.77	120.99	110.60
1	C	36	TRP	CB-CA-C	5.76	121.92	110.40
2	N	407	ARG	NE-CZ-NH1	5.76	123.18	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	74	ASP	CB-CG-OD1	5.74	123.47	118.30
1	A	166	ARG	CD-NE-CZ	5.73	131.62	123.60
1	C	146	ASP	CB-CG-OD1	5.73	123.46	118.30
2	N	413	ASP	CB-CG-OD2	-5.72	113.15	118.30
2	P	428	ARG	CB-CG-CD	5.72	126.46	111.60
1	A	146	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	E	64	ARG	CD-NE-CZ	-5.70	115.62	123.60
2	P	452	GLY	N-CA-C	-5.70	98.86	113.10
1	B	183	TYR	N-CA-CB	5.69	120.84	110.60
1	A	31	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	D	184	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	D	38	ARG	CD-NE-CZ	-5.66	115.68	123.60
2	P	372	LEU	CA-CB-CG	5.65	128.30	115.30
2	R	450	ARG	NE-CZ-NH1	5.65	123.12	120.30
1	A	65	ASP	CB-CG-OD1	5.65	123.38	118.30
1	A	147	ASP	CB-CG-OD2	-5.65	113.22	118.30
1	F	133	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	E	78	GLU	CA-CB-CG	5.62	125.76	113.40
2	O	428	ARG	CB-CG-CD	5.61	126.18	111.60
2	M	413	ASP	CB-CG-OD2	-5.61	113.25	118.30
2	P	531	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	E	184	ARG	NE-CZ-NH1	5.58	123.09	120.30
2	P	519	LEU	CB-CA-C	5.57	120.78	110.20
1	B	178	ASP	CB-CG-OD2	-5.56	113.30	118.30
2	M	528	ARG	NE-CZ-NH1	5.55	123.08	120.30
2	R	428	ARG	CG-CD-NE	5.54	123.43	111.80
1	A	19	ILE	CB-CA-C	5.53	122.67	111.60
1	D	175	CYS	CA-CB-SG	5.53	123.95	114.00
1	C	167	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	F	184	ARG	NE-CZ-NH2	-5.51	117.54	120.30
2	O	522	ARG	NE-CZ-NH2	5.51	123.06	120.30
1	B	74	ASP	CB-CG-OD1	5.51	123.26	118.30
1	D	81	ASP	CB-CG-OD1	5.51	123.26	118.30
2	R	432	ASP	CB-CG-OD2	-5.50	113.35	118.30
2	M	324	TYR	CB-CG-CD2	-5.49	117.71	121.00
2	O	447	TYR	N-CA-CB	-5.48	100.73	110.60
2	Q	415	TYR	CB-CA-C	5.48	121.36	110.40
2	N	428	ARG	CB-CG-CD	5.47	125.82	111.60
2	N	432	ASP	CB-CG-OD1	5.47	123.22	118.30
2	Q	360	ASP	CB-CG-OD2	-5.46	113.38	118.30
1	C	133	ARG	CA-CB-CG	5.46	125.41	113.40
2	Q	311	ARG	NE-CZ-NH2	-5.46	117.57	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	383	ARG	NE-CZ-NH2	-5.45	117.57	120.30
2	M	450	ARG	NE-CZ-NH1	5.45	123.02	120.30
1	A	78	GLU	CA-CB-CG	5.44	125.38	113.40
2	O	313	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	B	184	ARG	CD-NE-CZ	5.43	131.20	123.60
1	E	144	TYR	N-CA-CB	5.42	120.36	110.60
2	M	428	ARG	CB-CG-CD	5.42	125.68	111.60
2	M	330	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	E	184	ARG	NE-CZ-NH2	-5.41	117.59	120.30
2	R	450	ARG	NE-CZ-NH2	-5.41	117.59	120.30
2	Q	311	ARG	CD-NE-CZ	5.40	131.16	123.60
2	Q	361	HIS	CA-CB-CG	-5.40	104.42	113.60
1	A	64	ARG	CD-NE-CZ	-5.38	116.06	123.60
2	N	313	ARG	CD-NE-CZ	5.36	131.11	123.60
2	P	307	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	B	78	GLU	OE1-CD-OE2	5.36	129.73	123.30
2	R	361	HIS	CA-CB-CG	-5.35	104.50	113.60
1	C	166	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	B	166	ARG	NE-CZ-NH1	5.33	122.97	120.30
2	M	413	ASP	CB-CG-OD1	5.33	123.10	118.30
2	O	314	ASN	CB-CA-C	5.32	121.03	110.40
2	O	312	ASP	CB-CG-OD1	5.30	123.07	118.30
1	B	194	GLU	CA-CB-CG	5.29	125.05	113.40
2	O	434	ASP	CA-CB-CG	-5.29	101.75	113.40
1	C	184	ARG	CD-NE-CZ	-5.29	116.20	123.60
2	O	360	ASP	CB-CG-OD2	-5.27	113.56	118.30
2	P	506	ALA	CB-CA-C	5.27	118.01	110.10
2	R	524	ASP	CB-CG-OD1	5.27	123.05	118.30
1	B	186	ASP	CB-CG-OD2	-5.27	113.56	118.30
1	E	64	ARG	NE-CZ-NH1	-5.27	117.67	120.30
1	F	43	ASP	CB-CG-OD2	-5.25	113.57	118.30
1	D	52	LEU	CB-CA-C	5.24	120.16	110.20
2	O	323	ASP	CB-CG-OD1	5.24	123.02	118.30
2	P	323	ASP	CB-CG-OD1	5.24	123.01	118.30
1	A	69	GLU	CG-CD-OE2	5.23	128.76	118.30
2	N	416	LEU	CB-CA-C	5.20	120.08	110.20
1	D	133	ARG	N-CA-CB	-5.20	101.24	110.60
2	P	517	ASP	CB-CG-OD2	-5.18	113.63	118.30
1	C	174	ARG	NE-CZ-NH2	-5.18	117.71	120.30
1	F	23	LEU	CB-CA-C	5.18	120.04	110.20
2	Q	416	LEU	CB-CA-C	5.18	120.03	110.20
1	C	81	ASP	CB-CG-OD2	-5.17	113.65	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	416	LEU	CB-CA-C	5.17	120.02	110.20
2	N	376	GLU	CG-CD-OE2	-5.17	107.97	118.30
1	C	81	ASP	CB-CG-OD1	5.17	122.95	118.30
1	D	103	GLU	CG-CD-OE1	-5.16	107.97	118.30
2	M	383	ARG	NE-CZ-NH2	-5.16	117.72	120.30
2	N	451	ASN	CB-CA-C	5.16	120.72	110.40
1	D	186	ASP	CB-CG-OD1	5.15	122.94	118.30
1	B	57	ASP	CB-CG-OD1	5.14	122.93	118.30
1	E	133	ARG	NH1-CZ-NH2	5.14	125.05	119.40
1	A	169	THR	CA-CB-CG2	5.14	119.59	112.40
1	E	147	ASP	CB-CG-OD2	-5.13	113.68	118.30
1	E	43	ASP	CB-CG-OD2	-5.13	113.68	118.30
1	B	174	ARG	CD-NE-CZ	-5.13	116.42	123.60
2	P	531	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	D	86	GLU	CG-CD-OE1	5.12	128.54	118.30
2	N	360	ASP	CB-CG-OD2	-5.12	113.70	118.30
2	R	333	ARG	NE-CZ-NH1	5.11	122.86	120.30
2	P	428	ARG	CG-CD-NE	5.09	122.50	111.80
2	N	457	ARG	CG-CD-NE	5.09	122.49	111.80
1	C	57	ASP	CB-CG-OD1	5.09	122.88	118.30
2	Q	457	ARG	NE-CZ-NH1	5.07	122.84	120.30
2	R	414	ARG	NE-CZ-NH1	5.07	122.84	120.30
2	Q	360	ASP	CB-CG-OD1	5.07	122.86	118.30
2	Q	455	ASP	CB-CG-OD2	5.06	122.85	118.30
2	Q	452	GLY	N-CA-C	-5.05	100.47	113.10
1	B	64	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	A	23	LEU	CB-CA-C	5.04	119.79	110.20
2	N	522	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	D	69	GLU	CG-CD-OE2	5.04	128.39	118.30
1	B	65	ASP	CB-CG-OD2	-5.04	113.77	118.30
1	F	32	ASP	CB-CG-OD1	5.04	122.83	118.30
2	M	376	GLU	CG-CD-OE2	-5.04	108.23	118.30
2	N	413	ASP	CB-CG-OD1	5.03	122.83	118.30
2	R	307	ARG	NE-CZ-NH1	5.03	122.82	120.30
2	Q	386	ASP	CB-CA-C	5.02	120.45	110.40
2	Q	434	ASP	CA-CB-CG	-5.01	102.37	113.40
2	N	452	GLY	N-CA-C	-5.01	100.58	113.10
2	P	409	ARG	NE-CZ-NH2	-5.00	117.80	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	184	ARG	Sidechain
2	M	528	ARG	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1571	0	1499	44	0
1	B	1571	0	1499	43	0
1	C	1571	0	1499	47	0
1	D	1571	0	1499	37	0
1	E	1571	0	1499	40	0
1	F	1571	0	1499	61	0
2	M	1840	0	1793	60	0
2	N	1840	0	1793	32	0
2	O	1840	0	1793	50	0
2	P	1840	0	1793	44	0
2	Q	1840	0	1793	45	0
2	R	1840	0	1793	62	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	2	0
4	O	4	0	5	2	0
4	P	4	0	5	0	0
4	Q	4	0	5	2	0
4	R	4	0	5	0	0
5	M	11	0	3	0	0
5	N	11	0	3	0	0
5	O	11	0	3	0	0
5	P	11	0	3	0	0
5	Q	11	0	3	0	0
5	R	11	0	3	0	0
6	A	86	0	0	1	0
6	B	85	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	83	0	0	1	0
6	D	81	0	0	1	0
6	E	86	0	0	2	0
6	F	86	0	0	1	0
6	M	155	0	0	4	0
6	N	160	0	0	3	0
6	O	157	0	0	4	0
6	P	155	0	0	7	0
6	Q	161	0	0	5	0
6	R	157	0	0	4	0
All	All	22014	0	19800	515	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 (515) 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:E:165:GLN:H	1:E:165:GLN:NE2	1.44	1.14
1:C:64:ARG:NH1	1:C:100:ASP:O	1.82	1.13
1:E:165:GLN:HE21	1:E:165:GLN:N	1.50	1.09
1:B:165:GLN:H	1:B:165:GLN:NE2	1.50	1.07
1:D:64:ARG:NH1	1:D:100:ASP:O	1.94	1.01
2:P:364:LEU:HD22	2:P:440:ARG:HD3	1.39	0.98
1:F:168:GLU:HA	1:F:171:ILE:HD13	1.45	0.97
1:C:163:GLN:HB3	1:C:165:GLN:NE2	1.82	0.95
1:F:64:ARG:NH1	1:F:100:ASP:O	1.98	0.94
1:E:64:ARG:NH1	1:E:100:ASP:O	1.99	0.94
1:F:168:GLU:HA	1:F:171:ILE:CD1	1.96	0.94
2:M:497:ASN:ND2	2:M:499:GLU:H	1.66	0.93
2:R:497:ASN:ND2	2:R:499:GLU:H	1.65	0.92
1:F:165:GLN:H	1:F:165:GLN:NE2	1.66	0.92
2:M:364:LEU:HD22	2:M:440:ARG:HD3	1.53	0.91
1:A:64:ARG:NH1	1:A:100:ASP:O	2.03	0.90
2:N:390:LYS:HE2	6:N:824:HOH:O	1.73	0.88
1:B:176:GLU:HG3	1:B:180:LYS:O	1.73	0.88
2:Q:361:HIS:CD2	2:Q:361:HIS:H	1.93	0.87
2:R:497:ASN:HD22	2:R:499:GLU:H	1.21	0.87
1:F:176:GLU:HG3	1:F:180:LYS:O	1.76	0.86
1:E:168:GLU:HA	1:E:171:ILE:HD12	1.59	0.85
2:R:361:HIS:H	2:R:361:HIS:CD2	1.94	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:GLY:HA3	2:M:326:THR:HG22	1.59	0.85
1:A:163:GLN:HB3	1:A:165:GLN:NE2	1.91	0.85
1:F:165:GLN:H	1:F:165:GLN:HE21	1.23	0.85
2:N:390:LYS:HD3	6:N:746:HOH:O	1.77	0.84
1:B:163:GLN:HB3	1:B:165:GLN:HE22	1.43	0.82
2:R:390:LYS:HE2	6:R:861:HOH:O	1.80	0.82
1:A:19:ILE:HG22	1:A:26:ALA:HB1	1.61	0.81
1:B:165:GLN:NE2	1:B:165:GLN:N	2.28	0.81
1:B:163:GLN:HB3	1:B:165:GLN:NE2	1.95	0.81
1:C:163:GLN:HB3	1:C:165:GLN:HE22	1.45	0.79
1:D:165:GLN:H	1:D:165:GLN:HE21	1.30	0.78
1:C:176:GLU:OE2	1:C:179:GLY:HA2	1.84	0.78
1:A:176:GLU:HG3	1:A:180:LYS:O	1.85	0.77
1:C:176:GLU:HG3	1:C:180:LYS:O	1.84	0.77
2:M:361:HIS:H	2:M:361:HIS:CD2	2.01	0.77
2:M:497:ASN:HD22	2:M:499:GLU:H	1.31	0.77
1:B:19:ILE:HG22	1:B:26:ALA:HB1	1.66	0.77
2:Q:497:ASN:HD22	2:Q:499:GLU:H	1.32	0.77
1:B:64:ARG:NH1	1:B:100:ASP:O	2.18	0.77
2:P:364:LEU:CD2	2:P:440:ARG:HD3	2.15	0.76
1:F:49:ILE:HA	1:F:180:LYS:HE2	1.69	0.75
2:P:361:HIS:H	2:P:361:HIS:CD2	2.05	0.75
2:P:497:ASN:HD22	2:P:499:GLU:H	1.34	0.74
2:O:390:LYS:HE2	6:O:862:HOH:O	1.88	0.73
2:R:411:LYS:O	2:R:414:ARG:NH2	2.20	0.73
2:M:364:LEU:HD22	2:M:440:ARG:CD	2.19	0.72
1:E:24:GLU:HG3	6:E:781:HOH:O	1.89	0.72
1:F:131:PHE:CD2	2:R:475:ILE:HD12	2.24	0.72
1:F:98:THR:OG1	1:F:102:GLY:N	2.23	0.72
1:F:24:GLU:HG3	6:F:781:HOH:O	1.88	0.72
1:B:24:GLU:HG3	6:B:781:HOH:O	1.91	0.71
2:Q:361:HIS:H	2:Q:361:HIS:HD2	1.33	0.71
1:B:165:GLN:H	1:B:165:GLN:HE21	1.37	0.71
1:C:165:GLN:NE2	1:C:165:GLN:H	1.89	0.71
2:Q:390:LYS:HD2	6:Q:668:HOH:O	1.89	0.71
1:C:24:GLU:HG3	6:C:781:HOH:O	1.92	0.70
1:D:24:GLU:HG3	6:D:781:HOH:O	1.92	0.70
1:F:180:LYS:HG2	1:F:181:THR:N	2.06	0.70
2:N:497:ASN:HD22	2:N:499:GLU:H	1.39	0.70
2:R:505:ILE:HG22	2:R:507:LYS:HE3	1.73	0.70
1:A:176:GLU:OE2	1:A:179:GLY:HA2	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:GLU:HG3	6:A:663:HOH:O	1.91	0.69
2:P:497:ASN:ND2	2:P:499:GLU:H	1.90	0.69
2:P:361:HIS:H	2:P:361:HIS:HD2	1.39	0.69
1:D:98:THR:OG1	1:D:102:GLY:N	2.24	0.69
1:D:131:PHE:CD2	2:P:475:ILE:HD12	2.28	0.69
2:P:307:ARG:HG2	2:P:533:THR:HG22	1.74	0.69
2:M:315:TRP:HZ2	2:M:503:GLN:HE21	1.40	0.68
1:E:176:GLU:OE2	1:E:179:GLY:HA2	1.93	0.68
1:D:176:GLU:HG3	1:D:180:LYS:O	1.94	0.68
2:Q:497:ASN:ND2	2:Q:499:GLU:H	1.92	0.68
1:F:176:GLU:OE2	1:F:179:GLY:HA2	1.94	0.68
2:Q:315:TRP:HZ2	2:Q:503:GLN:HE21	1.43	0.67
2:R:416:LEU:C	2:R:416:LEU:HD23	2.15	0.67
1:B:165:GLN:H	1:B:165:GLN:CD	1.95	0.66
1:B:165:GLN:N	1:B:165:GLN:HE21	1.90	0.66
2:Q:361:HIS:CG	4:Q:601:BME:H21	2.30	0.66
1:C:78:GLU:HG2	2:O:301:PRO:CG	2.26	0.66
1:D:19:ILE:O	2:P:426:VAL:HG21	1.95	0.66
2:M:446:PRO:HD2	2:P:376:GLU:HG2	1.78	0.65
2:M:497:ASN:HD22	2:M:498:PRO:N	1.94	0.65
2:O:361:HIS:H	2:O:361:HIS:CD2	2.14	0.65
1:F:48:HIS:HA	1:F:109:VAL:HG12	1.77	0.65
2:R:497:ASN:ND2	2:R:499:GLU:OE1	2.27	0.65
2:O:497:ASN:HD22	2:O:499:GLU:H	1.46	0.64
2:M:497:ASN:HD22	2:M:497:ASN:C	2.00	0.64
2:R:361:HIS:H	2:R:361:HIS:HD2	1.40	0.64
1:E:64:ARG:HG2	1:E:64:ARG:HH11	1.62	0.64
2:M:361:HIS:H	2:M:361:HIS:HD2	1.40	0.63
1:A:163:GLN:HB3	1:A:165:GLN:HE22	1.63	0.63
2:R:326:THR:HG22	2:R:330:ARG:HD2	1.79	0.63
1:C:131:PHE:O	1:C:132:ALA:HB2	1.98	0.63
1:E:19:ILE:O	2:Q:426:VAL:HG21	1.98	0.63
2:O:356:PHE:CD2	2:O:428:ARG:HD3	2.34	0.63
2:N:361:HIS:CD2	2:N:361:HIS:H	2.16	0.62
2:R:406:GLY:O	2:R:447:TYR:HD2	1.81	0.62
2:O:361:HIS:CG	4:O:601:BME:H21	2.35	0.62
2:M:497:ASN:ND2	2:M:499:GLU:N	2.45	0.62
1:E:176:GLU:HG3	1:E:180:LYS:O	2.00	0.62
1:E:143:LEU:HD23	1:E:143:LEU:C	2.19	0.62
2:R:416:LEU:HD23	2:R:417:ALA:N	2.14	0.62
2:O:497:ASN:ND2	2:O:499:GLU:H	1.97	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:24:GLU:OE1	1:D:25:ALA:N	2.30	0.61
1:B:176:GLU:HG3	1:B:180:LYS:C	2.21	0.61
1:F:155:CYS:O	1:F:159:ASN:ND2	2.33	0.61
1:E:98:THR:O	1:E:102:GLY:HA2	2.01	0.60
2:Q:406:GLY:O	2:Q:447:TYR:HD1	1.85	0.60
1:F:49:ILE:CA	1:F:180:LYS:HE2	2.30	0.60
1:C:78:GLU:CG	2:O:301:PRO:HG2	2.30	0.60
2:O:416:LEU:C	2:O:416:LEU:HD23	2.21	0.60
2:O:406:GLY:O	2:O:447:TYR:HD1	1.84	0.60
2:Q:438:SER:O	4:Q:601:BME:H22	2.02	0.60
1:B:70:VAL:HG11	1:B:106:LEU:HD11	1.83	0.60
2:N:307:ARG:HG2	2:N:533:THR:HG22	1.83	0.59
2:O:326:THR:HG22	2:O:326:THR:O	2.02	0.59
1:E:131:PHE:CE2	1:E:138:HIS:HB3	2.37	0.59
2:M:376:GLU:OE1	6:M:639:HOH:O	2.16	0.59
1:B:70:VAL:HG11	1:B:106:LEU:CD1	2.33	0.59
1:D:165:GLN:H	1:D:165:GLN:NE2	1.98	0.59
2:P:376:GLU:O	2:P:442:ILE:HA	2.03	0.59
1:F:70:VAL:HG11	1:F:106:LEU:HD11	1.83	0.59
1:B:78:GLU:HG2	2:N:301:PRO:CG	2.33	0.59
1:E:132:ALA:HB3	1:E:135:ILE:HD12	1.84	0.59
1:D:153:ALA:HB3	1:D:154:LYS:HE3	1.84	0.59
1:D:77:GLY:O	1:D:114:VAL:HG12	2.03	0.58
1:A:65:ASP:OD2	1:A:133:ARG:HD3	2.03	0.58
2:R:473:LYS:HD2	2:R:474:LEU:N	2.18	0.58
1:C:54:GLN:HG3	1:C:184:ARG:NH2	2.19	0.58
1:B:98:THR:O	1:B:102:GLY:HA2	2.03	0.58
1:E:131:PHE:CD2	1:E:138:HIS:HB3	2.39	0.58
2:N:326:THR:HG22	2:N:330:ARG:HD2	1.86	0.58
1:B:3:GLU:HA	1:B:3:GLU:OE1	2.03	0.57
1:F:98:THR:O	1:F:102:GLY:HA2	2.04	0.57
1:F:50:LEU:O	1:F:182:ALA:HA	2.05	0.57
2:R:497:ASN:HD22	2:R:497:ASN:C	2.07	0.57
2:M:406:GLY:O	2:M:447:TYR:HD2	1.88	0.57
1:B:78:GLU:HG2	2:N:301:PRO:HG3	1.86	0.57
1:C:98:THR:O	1:C:102:GLY:HA2	2.05	0.57
2:O:356:PHE:CE2	2:O:428:ARG:HD3	2.40	0.57
2:R:400:TRP:HA	2:R:425:GLY:O	2.04	0.57
1:A:168:GLU:HA	1:A:171:ILE:HD12	1.87	0.57
2:M:315:TRP:HZ2	2:M:503:GLN:NE2	2.01	0.57
2:N:497:ASN:ND2	2:N:499:GLU:H	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:390:LYS:HD2	6:M:644:HOH:O	2.05	0.56
1:B:114:VAL:HG23	1:B:122:MET:HE2	1.88	0.56
1:C:99:PHE:HE2	2:O:411:LYS:HD2	1.70	0.56
1:F:19:ILE:HG22	1:F:26:ALA:HB1	1.86	0.56
1:B:131:PHE:CD2	1:B:138:HIS:HB3	2.40	0.56
2:P:406:GLY:O	2:P:447:TYR:HD1	1.89	0.56
2:P:497:ASN:ND2	2:P:499:GLU:HB2	2.19	0.56
1:B:39:LEU:HD11	1:B:93:GLY:HA3	1.88	0.56
1:C:98:THR:OG1	1:C:102:GLY:N	2.38	0.55
1:F:131:PHE:CE2	2:R:475:ILE:HD12	2.41	0.55
2:R:415:TYR:CE1	2:R:416:LEU:HD22	2.40	0.55
1:F:19:ILE:O	2:R:426:VAL:HG21	2.06	0.55
2:R:497:ASN:HD22	2:R:498:PRO:N	2.03	0.55
1:C:19:ILE:O	2:O:426:VAL:HG21	2.07	0.55
2:R:383:ARG:HD2	2:R:436:TYR:CZ	2.41	0.55
1:B:163:GLN:CB	1:B:165:GLN:HE22	2.17	0.55
1:A:98:THR:HB	1:A:100:ASP:OD1	2.07	0.55
2:Q:497:ASN:ND2	2:Q:499:GLU:OE1	2.34	0.55
1:F:24:GLU:OE1	1:F:25:ALA:N	2.39	0.55
2:Q:359:HIS:O	2:Q:366:ASN:HB3	2.06	0.54
1:A:15:PRO:HB3	1:A:133:ARG:HD2	1.90	0.54
1:C:78:GLU:HG2	2:O:301:PRO:HG2	1.87	0.54
2:Q:376:GLU:O	2:Q:442:ILE:HA	2.07	0.54
1:C:24:GLU:OE1	1:C:25:ALA:N	2.37	0.54
1:D:50:LEU:O	1:D:182:ALA:HA	2.08	0.54
2:N:361:HIS:H	2:N:361:HIS:HD2	1.54	0.54
1:A:134:GLY:HA3	2:M:326:THR:CG2	2.36	0.54
1:C:100:ASP:N	1:C:100:ASP:OD1	2.40	0.54
1:A:39:LEU:HD11	1:A:93:GLY:HA3	1.90	0.54
1:C:3:GLU:OE1	1:C:3:GLU:HA	2.07	0.54
2:R:399:MET:HA	2:R:462:HIS:O	2.08	0.54
1:A:100:ASP:OD1	1:A:100:ASP:N	2.40	0.54
1:A:180:LYS:HG2	1:A:181:THR:N	2.23	0.54
1:C:165:GLN:H	1:C:165:GLN:CD	2.10	0.54
1:D:100:ASP:OD1	1:D:100:ASP:N	2.40	0.54
1:A:165:GLN:CD	1:A:165:GLN:H	2.10	0.53
1:C:41:LYS:HD2	1:C:88:ALA:HA	1.89	0.53
1:B:50:LEU:O	1:B:182:ALA:HA	2.08	0.53
2:N:400:TRP:HA	2:N:425:GLY:O	2.08	0.53
1:C:65:ASP:OD2	1:C:133:ARG:HD3	2.08	0.53
1:B:69:GLU:HG2	1:B:94:ARG:HG2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:497:ASN:ND2	2:N:499:GLU:HB2	2.23	0.53
1:E:163:GLN:HB3	1:E:165:GLN:NE2	2.24	0.53
1:A:19:ILE:HG22	1:A:26:ALA:CB	2.33	0.53
2:R:497:ASN:HD22	2:R:499:GLU:N	1.99	0.53
1:A:163:GLN:HB3	1:A:165:GLN:HE21	1.69	0.53
1:C:39:LEU:HD11	1:C:93:GLY:HA3	1.90	0.53
2:M:376:GLU:HG2	2:P:446:PRO:HD2	1.90	0.53
1:F:131:PHE:O	1:F:132:ALA:HB2	2.08	0.53
2:M:359:HIS:O	2:M:366:ASN:HB3	2.10	0.52
2:Q:497:ASN:HD22	2:Q:499:GLU:N	2.04	0.52
2:M:335:ALA:HB2	2:O:328:ILE:HD12	1.90	0.52
1:F:176:GLU:HG3	1:F:180:LYS:C	2.28	0.52
1:B:19:ILE:HD11	2:N:408:TYR:HD1	1.74	0.52
2:N:406:GLY:O	2:N:447:TYR:HD1	1.93	0.52
2:P:400:TRP:HA	2:P:425:GLY:O	2.09	0.52
2:R:522:ARG:NE	2:R:524:ASP:OD1	2.38	0.52
2:O:326:THR:HG22	2:O:330:ARG:HD2	1.90	0.52
2:R:390:LYS:HG2	6:R:861:HOH:O	2.09	0.52
2:Q:361:HIS:CD2	2:Q:361:HIS:N	2.67	0.52
2:M:363:LEU:HD23	2:M:425:GLY:HA2	1.90	0.52
1:C:163:GLN:CB	1:C:165:GLN:HE22	2.20	0.52
1:D:147:ASP:OD2	1:D:174:ARG:NH1	2.42	0.52
2:R:486:ILE:HB	2:R:487:PRO:HD3	1.92	0.52
1:A:35:ILE:HD13	2:M:351:PHE:CE1	2.45	0.52
2:P:386:ASP:HA	2:P:527:LEU:O	2.10	0.52
1:A:19:ILE:HG21	2:M:410:HIS:HB2	1.92	0.52
1:A:78:GLU:HG2	2:M:301:PRO:HB3	1.91	0.52
2:M:390:LYS:CD	6:M:644:HOH:O	2.58	0.52
2:R:376:GLU:O	2:R:442:ILE:HA	2.10	0.52
2:M:364:LEU:CD2	2:M:440:ARG:HD3	2.34	0.51
2:Q:362:ASP:OD1	2:Q:440:ARG:HD3	2.09	0.51
2:M:360:ASP:OD2	2:M:428:ARG:HD2	2.10	0.51
2:N:488:MET:CE	1:C:1:PRO:HG3	2.40	0.51
1:D:155:CYS:HB3	1:D:158:LEU:HB2	1.91	0.51
2:P:497:ASN:HD22	2:P:497:ASN:C	2.14	0.51
2:R:536:GLU:HB2	6:R:840:HOH:O	2.10	0.51
2:N:359:HIS:O	2:N:366:ASN:HB3	2.10	0.51
2:M:448:PRO:HB2	2:P:516:MET:HA	1.92	0.51
1:E:29:PRO:O	6:E:807:HOH:O	2.19	0.51
1:D:78:GLU:CG	2:P:301:PRO:CG	2.89	0.51
1:D:176:GLU:HA	1:D:180:LYS:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:64:ARG:NH1	1:E:64:ARG:HG2	2.23	0.51
2:R:505:ILE:HG22	2:R:507:LYS:CE	2.38	0.51
2:M:405:GLY:HA3	6:M:647:HOH:O	2.11	0.51
2:M:356:PHE:CD1	2:M:428:ARG:HD3	2.46	0.50
1:F:70:VAL:HG11	1:F:106:LEU:CD1	2.41	0.50
2:R:361:HIS:CD2	2:R:361:HIS:N	2.69	0.50
2:O:356:PHE:HD2	2:O:428:ARG:CD	2.24	0.50
2:Q:394:ASN:O	6:Q:643:HOH:O	2.20	0.50
2:R:497:ASN:ND2	2:R:499:GLU:N	2.47	0.50
2:O:497:ASN:HD22	2:O:497:ASN:C	2.15	0.50
2:P:364:LEU:HD11	2:P:442:ILE:HG23	1.93	0.50
1:C:180:LYS:HG2	1:C:181:THR:N	2.27	0.50
2:P:359:HIS:O	2:P:366:ASN:HB3	2.11	0.50
2:M:306:SER:OG	2:M:530:GLN:NE2	2.35	0.50
2:O:382:GLY:HA3	2:O:523:PHE:O	2.12	0.50
2:P:390:LYS:HD2	6:P:682:HOH:O	2.11	0.50
2:P:497:ASN:HD22	2:P:499:GLU:N	2.08	0.50
1:B:114:VAL:HG23	1:B:122:MET:CE	2.41	0.50
1:F:144:TYR:CE2	1:F:158:LEU:HD22	2.46	0.50
2:O:326:THR:CG2	2:O:330:ARG:HD2	2.42	0.50
1:D:131:PHE:CD2	1:D:138:HIS:HB3	2.47	0.50
2:M:362:ASP:OD1	2:M:440:ARG:HD2	2.11	0.49
1:D:143:LEU:C	1:D:143:LEU:HD23	2.33	0.49
2:Q:497:ASN:ND2	2:Q:499:GLU:HB2	2.27	0.49
1:B:180:LYS:HG2	1:B:181:THR:N	2.27	0.49
1:C:176:GLU:OE2	1:C:179:GLY:CA	2.58	0.49
2:P:497:ASN:HD21	2:P:499:GLU:HB2	1.77	0.49
2:M:416:LEU:C	2:M:416:LEU:CD2	2.81	0.49
2:P:486:ILE:HB	2:P:487:PRO:HD3	1.94	0.49
2:R:405:GLY:HA3	6:R:787:HOH:O	2.13	0.49
1:B:20:GLY:O	1:B:21:LEU:HD23	2.12	0.49
2:R:315:TRP:HZ2	2:R:503:GLN:HE21	1.60	0.49
2:O:390:LYS:HD3	6:O:784:HOH:O	2.11	0.49
1:D:33:GLN:O	2:P:428:ARG:NH2	2.43	0.49
2:P:326:THR:O	2:P:326:THR:HG22	2.12	0.49
1:F:31:ARG:NH1	2:R:428:ARG:HG2	2.28	0.49
1:F:69:GLU:HG2	1:F:94:ARG:HG2	1.95	0.49
2:M:376:GLU:O	2:M:442:ILE:HA	2.13	0.49
1:E:176:GLU:HA	1:E:180:LYS:O	2.13	0.49
1:C:163:GLN:HB3	1:C:165:GLN:HE21	1.72	0.48
2:O:399:MET:HA	2:O:462:HIS:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:315:TRP:CZ2	2:M:503:GLN:NE2	2.80	0.48
2:M:356:PHE:HD1	2:M:428:ARG:HD3	1.78	0.48
1:E:24:GLU:OE1	1:E:25:ALA:N	2.46	0.48
2:M:434:ASP:HB3	2:M:436:TYR:CD2	2.48	0.48
2:O:400:TRP:HA	2:O:425:GLY:O	2.13	0.48
1:E:70:VAL:HG11	1:E:106:LEU:HD11	1.95	0.48
2:Q:362:ASP:OD1	2:Q:440:ARG:CD	2.62	0.48
1:A:50:LEU:O	1:A:182:ALA:HA	2.12	0.48
2:N:361:HIS:ND1	4:N:601:BME:H21	2.29	0.48
1:F:84:ASN:OD1	1:F:86:GLU:HB2	2.13	0.48
1:E:70:VAL:HG12	1:E:128:ILE:HG12	1.95	0.48
2:M:307:ARG:HG2	2:M:533:THR:HG22	1.95	0.48
2:M:497:ASN:HD22	2:M:499:GLU:N	2.05	0.48
2:O:356:PHE:CD2	2:O:428:ARG:CD	2.97	0.48
1:F:33:GLN:HG2	1:F:85:LEU:HD12	1.95	0.48
2:M:364:LEU:HB2	2:M:440:ARG:HD3	1.96	0.48
1:C:11:GLN:HB2	2:O:477:GLN:HG3	1.96	0.47
1:D:28:ASN:HB3	1:D:29:PRO:HD2	1.96	0.47
2:P:372:LEU:HA	2:P:373:PRO:HD3	1.83	0.47
1:F:18:HIS:CE1	1:F:99:PHE:HE1	2.32	0.47
1:F:171:ILE:HD12	1:F:171:ILE:H	1.78	0.47
1:F:171:ILE:HD12	1:F:171:ILE:N	2.29	0.47
1:B:132:ALA:HB3	1:B:135:ILE:HD12	1.95	0.47
1:A:176:GLU:HG3	1:A:180:LYS:C	2.34	0.47
1:B:143:LEU:C	1:B:143:LEU:HD23	2.34	0.47
2:P:478:LEU:C	2:P:478:LEU:HD23	2.34	0.47
2:Q:399:MET:HA	2:Q:462:HIS:O	2.14	0.47
1:F:176:GLU:OE2	1:F:179:GLY:CA	2.61	0.47
2:R:356:PHE:CD1	2:R:428:ARG:HD3	2.49	0.47
1:C:176:GLU:HG3	1:C:180:LYS:C	2.35	0.47
1:A:132:ALA:HB3	1:A:135:ILE:HD12	1.95	0.47
1:A:176:GLU:OE2	1:A:179:GLY:CA	2.61	0.47
2:M:316:HIS:HB3	2:M:317:PRO:HD2	1.95	0.47
2:M:383:ARG:NH2	2:M:434:ASP:OD1	2.47	0.47
1:B:78:GLU:CG	2:N:301:PRO:CG	2.93	0.47
2:N:416:LEU:HD23	2:N:416:LEU:C	2.35	0.47
1:C:18:HIS:CE1	1:C:99:PHE:HE1	2.32	0.47
2:O:385:VAL:O	2:O:526:VAL:HA	2.14	0.47
2:Q:364:LEU:HB2	2:Q:440:ARG:HD3	1.97	0.47
2:Q:453:PRO:HB2	2:R:310:ILE:HD12	1.96	0.47
2:R:383:ARG:NH2	2:R:391:PRO:HG3	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:PHE:CE2	1:B:138:HIS:HB3	2.50	0.47
1:D:15:PRO:HB3	1:D:133:ARG:HD2	1.96	0.47
1:F:99:PHE:HE2	2:R:411:LYS:HD2	1.80	0.47
1:A:143:LEU:C	1:A:143:LEU:HD23	2.34	0.47
1:C:19:ILE:HD11	2:O:408:TYR:HD2	1.79	0.47
2:O:326:THR:O	2:O:326:THR:CG2	2.63	0.47
1:E:165:GLN:H	1:E:165:GLN:HE21	0.65	0.47
1:F:100:ASP:OD1	1:F:100:ASP:N	2.47	0.47
1:A:176:GLU:HA	1:A:180:LYS:O	2.15	0.47
2:M:489:CYS:O	2:M:493:LYS:HE3	2.14	0.47
1:D:51:LEU:O	1:D:105:THR:HA	2.14	0.47
1:C:176:GLU:HA	1:C:180:LYS:O	2.15	0.46
2:P:405:GLY:HA3	6:P:685:HOH:O	2.15	0.46
2:Q:416:LEU:HD23	2:Q:416:LEU:C	2.35	0.46
1:F:39:LEU:HD11	1:F:93:GLY:HA3	1.98	0.46
2:R:489:CYS:HA	2:R:490:PRO:HD3	1.69	0.46
1:A:19:ILE:HG23	2:M:410:HIS:HD2	1.79	0.46
1:B:20:GLY:C	1:B:21:LEU:HD23	2.36	0.46
2:O:420:ASP:HA	2:O:421:PRO:HD2	1.73	0.46
2:Q:416:LEU:HD23	2:Q:417:ALA:N	2.29	0.46
2:R:315:TRP:HZ2	2:R:503:GLN:NE2	2.14	0.46
1:A:98:THR:O	1:A:102:GLY:HA2	2.15	0.46
1:E:98:THR:HB	1:E:100:ASP:OD1	2.15	0.46
1:A:24:GLU:OE1	1:A:25:ALA:N	2.46	0.46
1:E:165:GLN:NE2	1:E:165:GLN:N	2.30	0.46
1:C:50:LEU:O	1:C:182:ALA:HA	2.15	0.46
1:F:35:ILE:HD13	2:R:351:PHE:CE1	2.50	0.46
1:F:131:PHE:CE2	1:F:138:HIS:HB3	2.51	0.46
1:F:165:GLN:HE21	1:F:165:GLN:N	2.02	0.46
2:M:448:PRO:HD3	2:M:456:TRP:CZ3	2.51	0.46
1:E:180:LYS:CG	1:E:181:THR:N	2.79	0.46
1:D:153:ALA:CB	1:D:154:LYS:HE3	2.46	0.45
2:O:478:LEU:HD23	2:O:478:LEU:C	2.37	0.45
1:D:18:HIS:CE1	1:D:99:PHE:CE1	3.04	0.45
2:N:497:ASN:HA	2:N:498:PRO:HD2	1.87	0.45
1:A:18:HIS:CE1	1:A:99:PHE:HE1	2.34	0.45
1:A:70:VAL:HG11	1:A:106:LEU:HD11	1.98	0.45
2:N:373:PRO:HB3	2:N:423:PHE:HB2	1.99	0.45
2:P:360:ASP:OD2	2:P:428:ARG:NH1	2.42	0.45
1:E:65:ASP:OD2	1:E:133:ARG:HD3	2.17	0.45
1:D:163:GLN:HA	1:D:164:PRO:HD3	1.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:64:ARG:HH11	1:E:64:ARG:CG	2.23	0.45
1:E:70:VAL:HG11	1:E:106:LEU:CD1	2.47	0.45
1:A:54:GLN:HG2	1:A:102:GLY:O	2.16	0.45
2:N:361:HIS:CG	4:N:601:BME:H21	2.52	0.45
2:O:489:CYS:HA	2:O:490:PRO:HD3	1.69	0.45
2:Q:484:PRO:O	2:Q:487:PRO:HD2	2.16	0.45
1:A:25:ALA:O	2:M:411:LYS:NZ	2.48	0.45
1:C:143:LEU:HD23	1:C:143:LEU:C	2.37	0.45
2:O:315:TRP:HZ2	2:O:503:GLN:NE2	2.15	0.45
1:D:18:HIS:CE1	1:D:99:PHE:HE1	2.35	0.45
2:Q:364:LEU:HD22	2:Q:440:ARG:HD3	1.97	0.45
1:B:190:GLN:HG3	2:N:333:ARG:HG2	1.99	0.45
2:N:489:CYS:HA	2:N:490:PRO:HD3	1.83	0.45
2:Q:411:LYS:O	2:Q:414:ARG:NH2	2.43	0.45
2:O:376:GLU:O	2:O:442:ILE:HA	2.16	0.44
1:D:24:GLU:O	1:D:27:GLY:N	2.45	0.44
1:F:50:LEU:HD23	1:F:177:VAL:HB	1.98	0.44
1:F:115:ASN:HA	1:F:121:PRO:HA	1.99	0.44
2:M:495:ILE:CG2	2:M:500:ALA:HB3	2.47	0.44
2:Q:315:TRP:CZ2	2:Q:503:GLN:NE2	2.86	0.44
2:Q:362:ASP:OD1	2:Q:364:LEU:HB2	2.16	0.44
1:F:120:VAL:HA	1:F:121:PRO:HD3	1.81	0.44
1:A:163:GLN:HA	1:A:164:PRO:HD2	1.89	0.44
2:R:437:TYR:CD1	2:R:437:TYR:C	2.91	0.44
2:Q:489:CYS:O	2:Q:493:LYS:HE3	2.18	0.44
2:Q:536:GLU:HB2	6:Q:722:HOH:O	2.17	0.44
2:R:364:LEU:HB2	2:R:440:ARG:HD3	1.99	0.44
1:E:41:LYS:HD2	1:E:88:ALA:HA	1.99	0.44
2:Q:497:ASN:HD21	2:Q:499:GLU:HB2	1.83	0.44
2:O:486:ILE:N	2:O:487:PRO:HD2	2.33	0.44
1:D:65:ASP:OD2	1:D:133:ARG:HD3	2.18	0.44
1:E:176:GLU:OE2	1:E:179:GLY:CA	2.63	0.44
2:Q:405:GLY:HA3	6:Q:671:HOH:O	2.16	0.44
2:M:350:ASN:C	2:M:350:ASN:OD1	2.57	0.44
1:D:131:PHE:CE2	1:D:138:HIS:HB3	2.53	0.44
2:Q:315:TRP:HZ2	2:Q:503:GLN:NE2	2.10	0.44
1:C:99:PHE:CE2	2:O:411:LYS:HD2	2.52	0.43
1:E:84:ASN:O	1:E:87:ASN:HB2	2.18	0.43
1:F:65:ASP:OD2	1:F:133:ARG:HD3	2.18	0.43
2:R:371:GLY:N	2:R:422:ASN:ND2	2.66	0.43
1:A:20:GLY:C	1:A:21:LEU:HD23	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:8:THR:HA	1:E:9:PRO:HD3	1.85	0.43
2:Q:415:TYR:CE1	2:Q:416:LEU:HD22	2.53	0.43
2:R:434:ASP:HB3	2:R:436:TYR:CD2	2.53	0.43
1:A:131:PHE:CD2	1:A:138:HIS:HB3	2.54	0.43
2:O:438:SER:O	4:O:601:BME:H22	2.19	0.43
1:E:58:GLY:HA2	1:E:190:GLN:HB3	2.00	0.43
2:Q:407:ARG:HD3	2:Q:417:ALA:O	2.18	0.43
2:Q:420:ASP:HA	2:Q:421:PRO:HD2	1.81	0.43
2:Q:488:MET:CE	1:F:1:PRO:HG2	2.49	0.43
2:R:497:ASN:HA	2:R:498:PRO:HD3	1.76	0.43
1:A:78:GLU:HG2	2:M:301:PRO:CB	2.48	0.43
1:B:176:GLU:OE2	1:B:179:GLY:C	2.57	0.43
2:O:315:TRP:HZ2	2:O:503:GLN:HE21	1.67	0.43
2:O:390:LYS:HA	2:O:391:PRO:HD3	1.81	0.43
1:D:131:PHE:CE2	2:P:475:ILE:HD12	2.53	0.43
2:P:519:LEU:HD23	2:P:519:LEU:HA	1.95	0.43
1:E:176:GLU:HG3	1:E:180:LYS:C	2.39	0.43
1:F:80:GLN:O	1:F:91:SER:HB2	2.18	0.43
2:P:376:GLU:OE1	6:P:676:HOH:O	2.21	0.43
2:P:390:LYS:HE2	6:P:759:HOH:O	2.19	0.43
2:P:307:ARG:HD2	6:P:695:HOH:O	2.19	0.43
2:Q:522:ARG:NH1	6:Q:690:HOH:O	2.51	0.43
1:F:33:GLN:HB3	1:F:85:LEU:HD11	2.01	0.43
2:R:488:MET:C	2:R:493:LYS:HE2	2.39	0.43
1:E:110:LYS:NZ	1:E:147:ASP:OD1	2.46	0.42
2:R:326:THR:CG2	2:R:330:ARG:HD2	2.45	0.42
2:R:505:ILE:O	2:R:507:LYS:HE3	2.19	0.42
1:A:114:VAL:HG23	1:A:122:MET:CE	2.49	0.42
2:O:497:ASN:HA	2:O:498:PRO:HD2	1.90	0.42
1:C:158:LEU:HD12	1:C:158:LEU:HA	1.82	0.42
2:O:359:HIS:O	2:O:366:ASN:HB3	2.19	0.42
1:D:163:GLN:HG3	1:F:61:HIS:ND1	2.34	0.42
1:E:50:LEU:O	1:E:182:ALA:HA	2.20	0.42
1:F:51:LEU:O	1:F:105:THR:HA	2.19	0.42
1:B:64:ARG:HD3	1:B:99:PHE:O	2.19	0.42
1:C:155:CYS:HB3	1:C:158:LEU:HB2	2.01	0.42
2:O:495:ILE:CG2	2:O:500:ALA:HB3	2.50	0.42
2:Q:364:LEU:HD22	2:Q:440:ARG:CD	2.48	0.42
1:F:134:GLY:HA3	2:R:326:THR:HG22	2.00	0.42
2:M:489:CYS:HA	2:M:490:PRO:HD3	1.74	0.42
2:O:406:GLY:O	2:O:447:TYR:CD1	2.69	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:411:LYS:H	2:P:411:LYS:HG3	1.56	0.42
1:E:100:ASP:OD1	1:E:100:ASP:N	2.52	0.42
1:F:168:GLU:CA	1:F:171:ILE:CD1	2.83	0.42
1:A:158:LEU:HD12	1:A:158:LEU:HA	1.90	0.42
1:A:165:GLN:NE2	1:A:165:GLN:H	2.17	0.42
1:B:168:GLU:HA	1:B:171:ILE:HD12	2.01	0.42
1:C:35:ILE:HG21	1:C:92:PHE:HE2	1.83	0.42
1:C:52:LEU:CD2	1:C:184:ARG:NH1	2.82	0.42
1:D:176:GLU:HG3	1:D:180:LYS:C	2.38	0.42
2:P:363:LEU:HD23	2:P:425:GLY:HA2	2.00	0.42
2:N:392:VAL:HG12	2:N:395:THR:HB	2.01	0.42
1:D:78:GLU:HG2	2:P:301:PRO:CG	2.50	0.42
2:P:497:ASN:HA	2:P:498:PRO:HD2	1.75	0.42
1:B:61:HIS:ND1	1:C:163:GLN:HG3	2.35	0.42
2:P:522:ARG:NH1	6:P:706:HOH:O	2.53	0.42
1:E:84:ASN:OD1	1:E:86:GLU:HB2	2.20	0.42
1:F:176:GLU:OE2	1:F:179:GLY:C	2.58	0.42
2:R:378:ILE:HA	2:R:519:LEU:O	2.20	0.42
2:M:420:ASP:HA	2:M:421:PRO:HD2	1.74	0.42
1:C:131:PHE:O	1:C:132:ALA:CB	2.65	0.42
2:O:364:LEU:HD22	2:O:440:ARG:CD	2.50	0.42
1:F:33:GLN:CG	1:F:85:LEU:HD12	2.49	0.42
1:F:54:GLN:HG3	1:F:184:ARG:NH2	2.35	0.42
2:R:307:ARG:NE	2:R:536:GLU:OE2	2.48	0.42
2:R:359:HIS:O	2:R:366:ASN:HB3	2.20	0.42
2:R:416:LEU:C	2:R:416:LEU:CD2	2.88	0.42
1:A:131:PHE:CD2	2:M:475:ILE:HD12	2.54	0.42
2:M:478:LEU:HD23	2:M:478:LEU:C	2.41	0.42
1:C:31:ARG:HB3	6:O:835:HOH:O	2.19	0.42
2:Q:413:ASP:O	2:Q:414:ARG:CZ	2.68	0.42
2:Q:522:ARG:NE	2:Q:524:ASP:OD1	2.50	0.42
2:R:522:ARG:HH11	2:R:522:ARG:HD3	1.34	0.42
1:A:114:VAL:HG23	1:A:122:MET:HE2	2.01	0.41
2:M:497:ASN:HA	2:M:498:PRO:HD2	1.66	0.41
2:N:486:ILE:N	2:N:487:PRO:HD2	2.35	0.41
1:C:79:TYR:O	2:O:301:PRO:HB3	2.19	0.41
2:M:497:ASN:ND2	2:M:499:GLU:HB2	2.35	0.41
2:N:399:MET:HA	2:N:462:HIS:O	2.21	0.41
1:F:176:GLU:HA	1:F:180:LYS:O	2.19	0.41
1:B:70:VAL:CG1	1:B:106:LEU:HD11	2.50	0.41
2:O:405:GLY:HA3	6:O:787:HOH:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:416:LEU:C	2:O:416:LEU:CD2	2.89	0.41
2:P:497:ASN:HD22	2:P:498:PRO:N	2.18	0.41
1:E:62:LEU:HD13	1:E:101:ALA:O	2.20	0.41
2:M:372:LEU:HA	2:M:373:PRO:HD3	1.89	0.41
1:B:120:VAL:HA	1:B:121:PRO:HD3	1.95	0.41
2:O:411:LYS:H	2:O:411:LYS:HG3	1.64	0.41
1:D:63:VAL:HG12	1:D:66:SER:HB3	2.03	0.41
1:D:140:HIS:O	1:D:197:PHE:HA	2.20	0.41
1:B:15:PRO:HB3	1:B:133:ARG:HD2	2.02	0.41
2:N:405:GLY:HA3	6:N:749:HOH:O	2.20	0.41
2:O:356:PHE:HD2	2:O:428:ARG:HD2	1.84	0.41
1:D:180:LYS:HG2	1:D:181:THR:N	2.36	0.41
1:F:19:ILE:O	2:R:426:VAL:CG2	2.67	0.41
1:B:195:THR:HG22	1:B:196:VAL:O	2.21	0.41
2:N:315:TRP:HZ2	2:N:503:GLN:HE21	1.68	0.41
2:Q:372:LEU:HA	2:Q:373:PRO:HD3	1.94	0.41
2:R:363:LEU:HD12	2:R:363:LEU:N	2.36	0.41
2:N:489:CYS:O	2:N:493:LYS:HE3	2.21	0.41
2:Q:400:TRP:HA	2:Q:425:GLY:O	2.21	0.41
1:F:165:GLN:NE2	1:F:165:GLN:N	2.50	0.41
2:R:478:LEU:C	2:R:478:LEU:HD23	2.41	0.41
1:B:133:ARG:NH2	1:C:162:GLU:OE2	2.51	0.41
2:O:361:HIS:H	2:O:361:HIS:HD2	1.66	0.41
1:E:51:LEU:HD11	1:E:126:ILE:HD12	2.02	0.41
1:F:99:PHE:CE2	2:R:411:LYS:HD2	2.55	0.41
2:M:495:ILE:HG21	2:M:500:ALA:HB3	2.03	0.41
2:M:497:ASN:HD21	2:M:499:GLU:HB2	1.86	0.41
2:M:500:ALA:O	2:M:503:GLN:HB2	2.21	0.41
2:R:364:LEU:HD22	2:R:440:ARG:HD3	2.02	0.41
2:N:497:ASN:HD22	2:N:497:ASN:C	2.24	0.40
1:C:2:ILE:HA	1:C:2:ILE:HD13	1.83	0.40
2:P:326:THR:O	2:P:326:THR:CG2	2.69	0.40
2:Q:486:ILE:HB	2:Q:487:PRO:HD3	2.03	0.40
2:M:361:HIS:CD2	2:M:361:HIS:N	2.74	0.40
1:F:78:GLU:CG	2:R:301:PRO:CG	2.99	0.40
1:F:147:ASP:OD2	1:F:174:ARG:NH1	2.49	0.40
2:N:457:ARG:HA	2:N:458:PRO:HD3	1.93	0.40
2:R:497:ASN:ND2	2:R:499:GLU:HB2	2.36	0.40
1:C:30:THR:HB	1:C:34:GLU:HG3	2.03	0.40
2:P:450:ARG:HG3	6:P:673:HOH:O	2.21	0.40
1:F:160:LEU:HD23	1:F:160:LEU:HA	1.89	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 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%)	193 (98%)	5 (2%)	0	100	100
1	B	198/200 (99%)	192 (97%)	6 (3%)	0	100	100
1	C	198/200 (99%)	190 (96%)	8 (4%)	0	100	100
1	D	198/200 (99%)	189 (96%)	9 (4%)	0	100	100
1	E	198/200 (99%)	191 (96%)	7 (4%)	0	100	100
1	F	198/200 (99%)	191 (96%)	6 (3%)	1 (0%)	29	22
2	M	229/238 (96%)	220 (96%)	9 (4%)	0	100	100
2	N	229/238 (96%)	221 (96%)	8 (4%)	0	100	100
2	O	229/238 (96%)	218 (95%)	11 (5%)	0	100	100
2	P	229/238 (96%)	222 (97%)	7 (3%)	0	100	100
2	Q	229/238 (96%)	223 (97%)	6 (3%)	0	100	100
2	R	229/238 (96%)	220 (96%)	9 (4%)	0	100	100
All	All	2562/2628 (98%)	2470 (96%)	91 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	132	ALA

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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%)	153 (94%)	9 (6%)	21	16
1	B	162/163 (99%)	153 (94%)	9 (6%)	21	16
1	C	162/163 (99%)	151 (93%)	11 (7%)	16	10
1	D	162/163 (99%)	153 (94%)	9 (6%)	21	16
1	E	162/163 (99%)	155 (96%)	7 (4%)	29	25
1	F	162/163 (99%)	153 (94%)	9 (6%)	21	16
2	M	196/202 (97%)	183 (93%)	13 (7%)	16	11
2	N	196/202 (97%)	186 (95%)	10 (5%)	24	19
2	O	196/202 (97%)	186 (95%)	10 (5%)	24	19
2	P	196/202 (97%)	184 (94%)	12 (6%)	18	13
2	Q	196/202 (97%)	185 (94%)	11 (6%)	21	16
2	R	196/202 (97%)	185 (94%)	11 (6%)	21	16
All	All	2148/2190 (98%)	2027 (94%)	121 (6%)	21	16

All (121) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	19	ILE
1	A	24	GLU
1	A	38	ARG
1	A	52	LEU
1	A	100	ASP
1	A	158	LEU
1	A	165	GLN
1	A	192	GLU
2	M	301	PRO
2	M	372	LEU
2	M	395	THR
2	M	399	MET
2	M	411	LYS
2	M	416	LEU
2	M	428	ARG
2	M	434	ASP
2	M	440	ARG
2	M	478	LEU
2	M	497	ASN

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Mol	Chain	Res	Type
2	M	507	LYS
2	M	534	HIS
1	B	4	LEU
1	B	19	ILE
1	B	24	GLU
1	B	38	ARG
1	B	52	LEU
1	B	141	THR
1	B	164	PRO
1	B	165	GLN
1	B	192	GLU
2	N	364	LEU
2	N	372	LEU
2	N	395	THR
2	N	399	MET
2	N	411	LYS
2	N	416	LEU
2	N	428	ARG
2	N	497	ASN
2	N	507	LYS
2	N	534	HIS
1	C	4	LEU
1	C	19	ILE
1	C	24	GLU
1	C	38	ARG
1	C	52	LEU
1	C	66	SER
1	C	100	ASP
1	C	158	LEU
1	C	165	GLN
1	C	181	THR
1	C	192	GLU
2	O	372	LEU
2	O	393	PRO
2	O	395	THR
2	O	399	MET
2	O	411	LYS
2	O	416	LEU
2	O	434	ASP
2	O	478	LEU
2	O	497	ASN
2	O	534	HIS

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Mol	Chain	Res	Type
1	D	4	LEU
1	D	19	ILE
1	D	24	GLU
1	D	38	ARG
1	D	52	LEU
1	D	100	ASP
1	D	154	LYS
1	D	165	GLN
1	D	192	GLU
2	P	364	LEU
2	P	372	LEU
2	P	395	THR
2	P	399	MET
2	P	411	LYS
2	P	416	LEU
2	P	428	ARG
2	P	434	ASP
2	P	478	LEU
2	P	497	ASN
2	P	503	GLN
2	P	534	HIS
1	E	19	ILE
1	E	24	GLU
1	E	38	ARG
1	E	52	LEU
1	E	100	ASP
1	E	165	GLN
1	E	192	GLU
2	Q	306	SER
2	Q	372	LEU
2	Q	395	THR
2	Q	399	MET
2	Q	416	LEU
2	Q	428	ARG
2	Q	434	ASP
2	Q	442	ILE
2	Q	497	ASN
2	Q	507	LYS
2	Q	534	HIS
1	F	4	LEU
1	F	19	ILE
1	F	24	GLU

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Mol	Chain	Res	Type
1	F	52	LEU
1	F	78	GLU
1	F	91	SER
1	F	100	ASP
1	F	165	GLN
1	F	192	GLU
2	R	372	LEU
2	R	383	ARG
2	R	395	THR
2	R	399	MET
2	R	411	LYS
2	R	416	LEU
2	R	428	ARG
2	R	434	ASP
2	R	497	ASN
2	R	503	GLN
2	R	534	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) 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
2	M	530	GLN
1	B	165	GLN
2	N	361	HIS
2	N	412	ASN
2	N	497	ASN
2	N	503	GLN
1	C	165	GLN
2	O	361	HIS
2	O	412	ASN
2	O	497	ASN
2	O	503	GLN
1	D	165	GLN
2	P	361	HIS
2	P	412	ASN
2	P	497	ASN

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Mol	Chain	Res	Type
2	P	503	GLN
1	E	165	GLN
2	Q	361	HIS
2	Q	412	ASN
2	Q	497	ASN
2	Q	503	GLN
1	F	163	GLN
1	F	165	GLN
2	R	361	HIS
2	R	422	ASN
2	R	497	ASN
2	R	503	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 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	BME	M	601	2	3,3,3	0.43	0	1,2,2	0.64	0
4	BME	R	601	2	3,3,3	0.48	0	1,2,2	0.19	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BME	O	601	2	3,3,3	0.47	0	1,2,2	0.97	0
5	NNO	R	550	3	9,11,11	1.40	2 (22%)	9,15,15	1.45	2 (22%)
5	NNO	M	550	3	9,11,11	1.63	4 (44%)	9,15,15	1.46	1 (11%)
5	NNO	N	550	3	9,11,11	1.59	4 (44%)	9,15,15	1.37	2 (22%)
5	NNO	P	550	3	9,11,11	1.55	2 (22%)	9,15,15	1.49	2 (22%)
5	NNO	O	550	3	9,11,11	1.60	4 (44%)	9,15,15	1.60	2 (22%)
4	BME	Q	601	2	3,3,3	0.77	0	1,2,2	0.94	0
5	NNO	Q	550	3	9,11,11	1.60	3 (33%)	9,15,15	1.33	2 (22%)
4	BME	N	601	2	3,3,3	0.25	0	1,2,2	0.47	0
4	BME	P	601	2	3,3,3	0.57	0	1,2,2	0.91	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
4	BME	M	601	2	-	0/1/1/1	-
4	BME	R	601	2	-	0/1/1/1	-
4	BME	O	601	2	-	0/1/1/1	-
5	NNO	R	550	3	-	0/4/4/4	0/1/1/1
5	NNO	M	550	3	-	0/4/4/4	0/1/1/1
5	NNO	N	550	3	-	0/4/4/4	0/1/1/1
5	NNO	P	550	3	-	0/4/4/4	0/1/1/1
5	NNO	O	550	3	-	0/4/4/4	0/1/1/1
4	BME	Q	601	2	-	0/1/1/1	-
5	NNO	Q	550	3	-	0/4/4/4	0/1/1/1
4	BME	N	601	2	-	0/1/1/1	-
4	BME	P	601	2	-	0/1/1/1	-

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	P	550	NNO	C3-C7	3.23	1.56	1.49
5	Q	550	NNO	C2-C3	2.99	1.43	1.39
5	M	550	NNO	C2-C3	2.50	1.42	1.39
5	N	550	NNO	C3-C7	2.47	1.54	1.49
5	O	550	NNO	C2-C3	2.42	1.42	1.39
5	M	550	NNO	C3-C7	2.38	1.54	1.49
5	O	550	NNO	C3-C7	2.33	1.54	1.49
5	M	550	NNO	O2-C7	-2.32	1.23	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	P	550	NNO	O2-C7	-2.30	1.23	1.30
5	N	550	NNO	C2-C3	2.15	1.42	1.39
5	Q	550	NNO	O2-C7	-2.15	1.24	1.30
5	R	550	NNO	C3-C7	2.14	1.54	1.49
5	N	550	NNO	O2-C7	-2.13	1.24	1.30
5	O	550	NNO	O2-C7	-2.13	1.24	1.30
5	Q	550	NNO	C3-C7	2.08	1.53	1.49
5	M	550	NNO	C2-N1	-2.08	1.31	1.35
5	R	550	NNO	O2-C7	-2.06	1.24	1.30
5	O	550	NNO	C2-N1	-2.03	1.31	1.35
5	N	550	NNO	C2-N1	-2.02	1.31	1.35

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	O	550	NNO	O2-C7-C3	3.06	122.79	114.85
5	M	550	NNO	O2-C7-C3	2.89	122.34	114.85
5	P	550	NNO	O2-C7-C3	2.71	121.88	114.85
5	R	550	NNO	O2-C7-O1	-2.63	117.50	123.35
5	O	550	NNO	O2-C7-O1	-2.62	117.53	123.35
5	P	550	NNO	O2-C7-O1	-2.60	117.57	123.35
5	N	550	NNO	O2-C7-C3	2.50	121.34	114.85
5	R	550	NNO	O2-C7-C3	2.28	120.77	114.85
5	Q	550	NNO	O2-C7-C3	2.28	120.77	114.85
5	Q	550	NNO	O2-C7-O1	-2.28	118.29	123.35
5	N	550	NNO	O2-C7-O1	-2.17	118.54	123.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	O	601	BME	2	0
4	Q	601	BME	2	0
4	N	601	BME	2	0

5.7 Other polymers [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.