



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 04:50 pm BST

PDB ID : 2W6F
Title : Low resolution structures of bovine mitochondrial F1-ATPase during controlled dehydration: Hydration State 2.
Authors : Sanchez-Weatherby, J.; Felisaz, F.; Gobbo, A.; Huet, J.; Ravelli, R.B.G.; Bowler, M.W.; Cipriani, F.
Deposited on : 2008-12-18
Resolution : 6.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

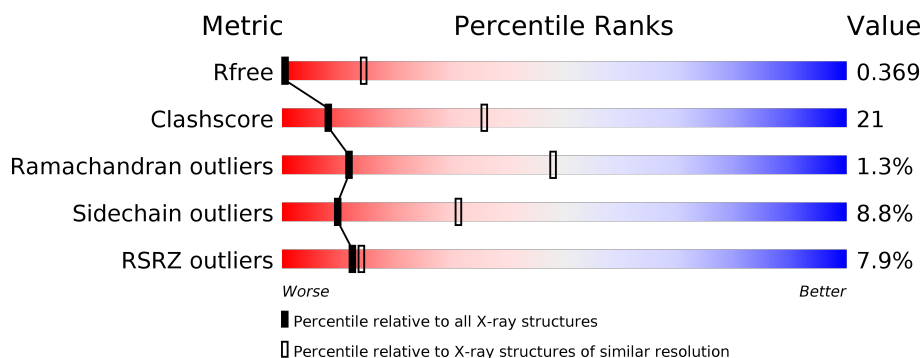
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 6.00 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))
R_{free}	130704	1000 (8.00-3.88)
Clashscore	141614	1049 (8.00-3.90)
Ramachandran outliers	138981	1016 (8.00-3.86)
Sidechain outliers	138945	1017 (8.00-3.82)
RSRZ outliers	127900	1015 (8.20-3.78)

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 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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	553	<div> <div>8%</div> <div> <div>47%</div> <div>33%</div> <div>7%</div> <div>12%</div> </div> </div>
1	B	553	<div> <div>5%</div> <div> <div>47%</div> <div>33%</div> <div>6%</div> <div>13%</div> </div> </div>
1	C	553	<div> <div>4%</div> <div> <div>52%</div> <div>32%</div> <div>•</div> <div>11%</div> </div> </div>
2	D	528	<div> <div>8%</div> <div> <div>53%</div> <div>30%</div> <div>5%</div> <div>12%</div> </div> </div>
2	E	528	<div> <div>12%</div> <div> <div>44%</div> <div>38%</div> <div>5%</div> <div>12%</div> </div> </div>
2	F	528	<div> <div>4%</div> <div> <div>56%</div> <div>29%</div> <div>•</div> <div>12%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	G	298	<div><div><div></div><div></div><div></div><div></div><div></div></div><div>4%20%17%. .59%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22663 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 ATP SYNTHASE SUBUNIT ALPHA HEART ISOFORM, MITOCHONDRIAL.

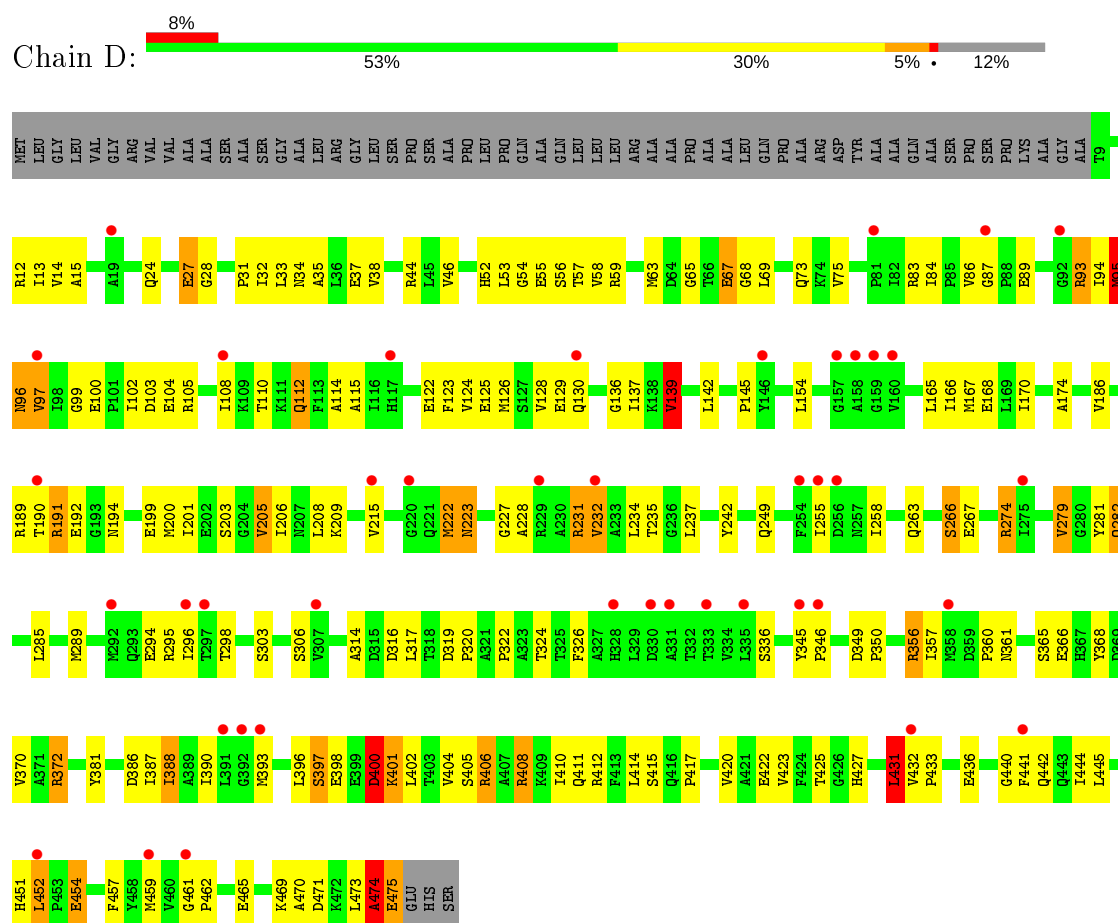
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	487	Total	C	N	O	S	0	0	0
			3715	2341	656	706	12			
1	B	479	Total	C	N	O	S	0	0	0
			3656	2303	647	694	12			
1	C	492	Total	C	N	O	S	0	0	0
			3748	2360	661	715	12			

- Molecule 2 is a protein called ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL.

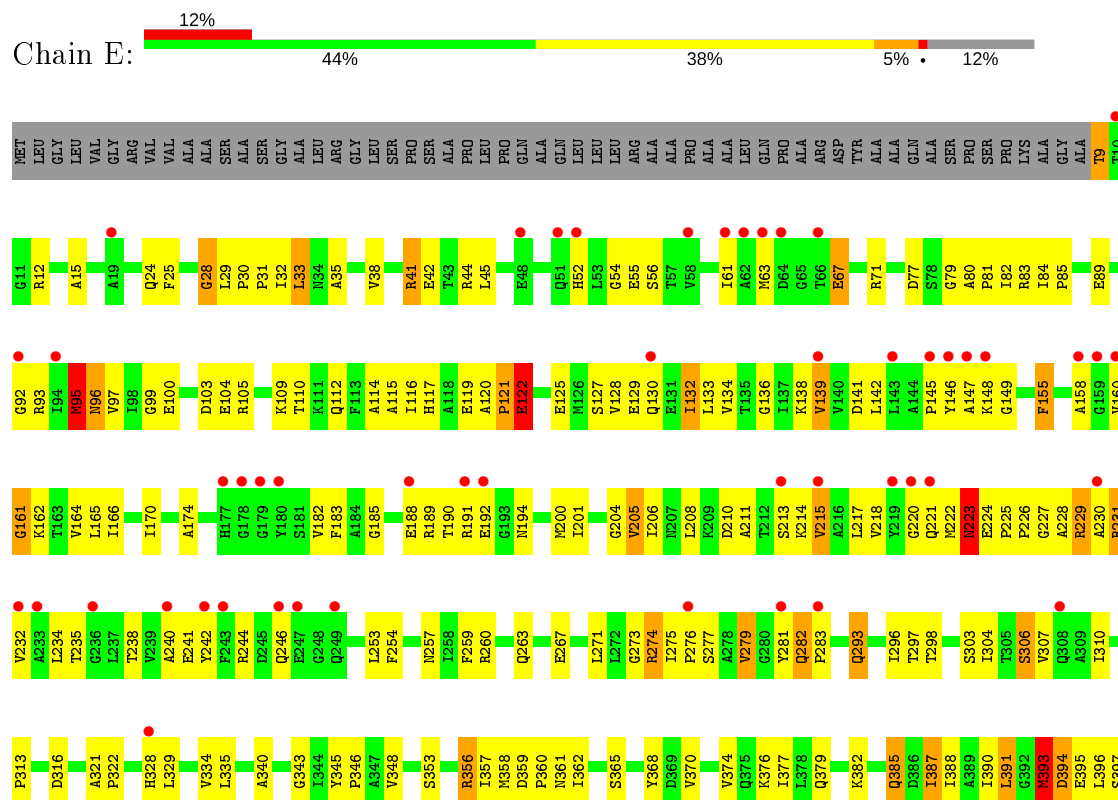
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	467	Total	C	N	O	S	0	0	0
			3539	2243	601	684	11			
2	E	466	Total	C	N	O	S	0	0	0
			3530	2238	600	681	11			
2	F	466	Total	C	N	O	S	0	0	0
			3530	2238	600	681	11			

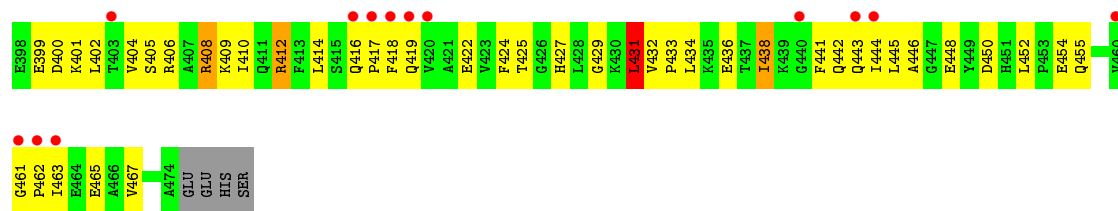
- Molecule 3 is a protein called ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	122	Total	C	N	O	S	0	0	0
			945	591	171	176	7			

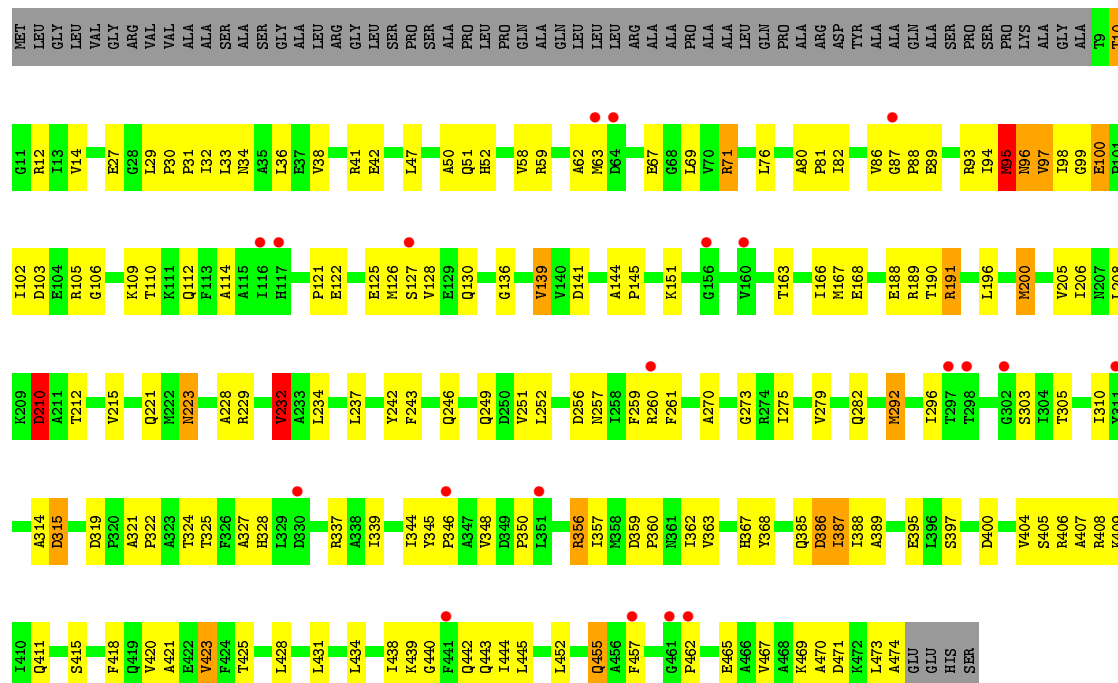


• Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

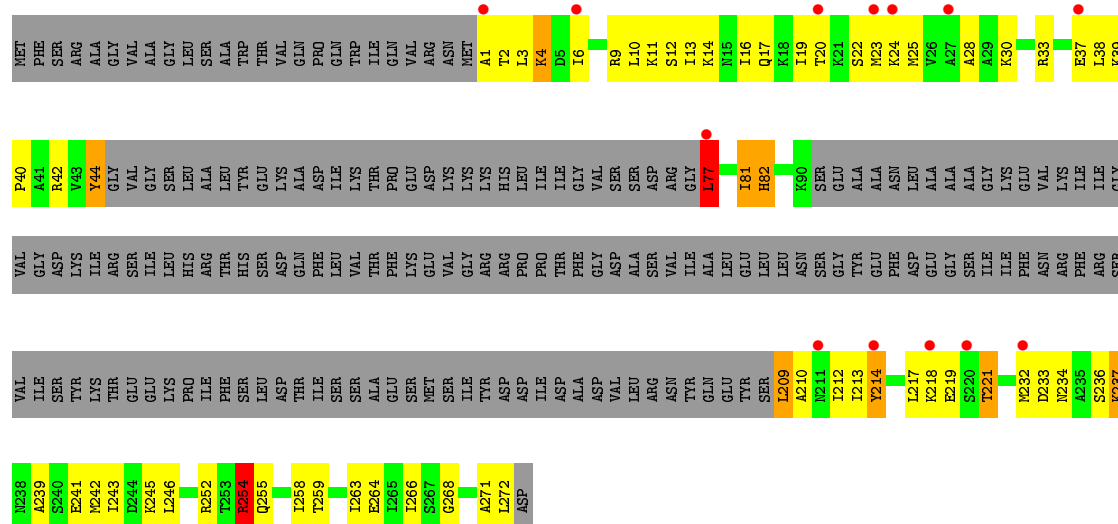




• Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL



• Molecule 3: ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	108.00 Å 139.53 Å 280.90 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 6.00 100.81 – 6.00	Depositor EDS
% Data completeness (in resolution range)	83.0 (30.00-6.00) 82.8 (100.81-6.00)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 6.19 Å)	Xtriage
Refinement program	REFMAC 5.5.0038	Depositor
R, R_{free}	0.345 , 0.343 0.355 , 0.369	Depositor DCC
R_{free} test set	445 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	152.7	Xtriage
Anisotropy	0.430	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 50.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.32$, $\langle L^2 \rangle = 0.15$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.66	EDS
Total number of atoms	22663	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.60	0/3766	1.31	29/5080 (0.6%)
1	B	0.60	0/3704	1.36	34/4995 (0.7%)
1	C	0.62	0/3799	1.38	25/5126 (0.5%)
2	D	0.62	0/3596	1.36	23/4879 (0.5%)
2	E	0.60	0/3587	1.32	18/4867 (0.4%)
2	F	0.62	0/3587	1.36	29/4867 (0.6%)
3	G	0.52	0/949	1.14	5/1266 (0.4%)
All	All	0.61	0/22988	1.34	163/31080 (0.5%)

There are no bond length outliers.

All (163) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	408	ARG	CD-NE-CZ	23.27	156.19	123.60
2	E	408	ARG	CD-NE-CZ	13.99	143.19	123.60
1	C	291	ARG	NE-CZ-NH2	-13.36	113.62	120.30
1	B	40	ARG	NE-CZ-NH1	13.03	126.82	120.30
1	B	279	ARG	NE-CZ-NH1	13.00	126.80	120.30
2	F	356	ARG	NE-CZ-NH1	11.54	126.07	120.30
2	D	406	ARG	NE-CZ-NH1	-11.46	114.57	120.30
2	F	59	ARG	NE-CZ-NH1	-11.38	114.61	120.30
2	D	408	ARG	NE-CZ-NH1	10.99	125.80	120.30
3	G	254	ARG	NE-CZ-NH2	-10.92	114.84	120.30
1	B	219	ARG	NE-CZ-NH2	10.55	125.58	120.30
2	F	282	GLN	CB-CG-CD	10.31	138.40	111.60
1	C	164	ARG	NE-CZ-NH1	-10.00	115.30	120.30
1	C	258	ARG	NE-CZ-NH1	10.00	125.30	120.30
1	B	40	ARG	CD-NE-CZ	9.89	137.45	123.60
2	F	229	ARG	NE-CZ-NH1	-9.49	115.55	120.30
2	F	356	ARG	NE-CZ-NH2	-9.40	115.60	120.30
2	D	44	ARG	NE-CZ-NH2	-9.27	115.67	120.30
2	F	95	MET	CA-CB-CG	9.22	128.98	113.30
1	B	304	ARG	NE-CZ-NH1	-9.15	115.72	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	161	ARG	NE-CZ-NH1	8.95	124.78	120.30
2	F	59	ARG	NE-CZ-NH2	8.94	124.77	120.30
1	A	420	ARG	NE-CZ-NH1	-8.79	115.91	120.30
1	C	450	ARG	NE-CZ-NH2	-8.75	115.93	120.30
2	F	96	ASN	CB-CA-C	-8.53	93.34	110.40
2	E	260	ARG	NE-CZ-NH1	-8.51	116.05	120.30
2	E	95	MET	CA-CB-CG	8.49	127.74	113.30
2	E	83	ARG	NE-CZ-NH1	-8.45	116.07	120.30
1	A	450	ARG	NE-CZ-NH2	-8.28	116.16	120.30
1	A	373	ARG	NE-CZ-NH2	8.19	124.39	120.30
1	A	398	ARG	NE-CZ-NH1	-8.18	116.21	120.30
1	C	127	ARG	NE-CZ-NH1	-8.06	116.27	120.30
2	F	229	ARG	NE-CZ-NH2	8.05	124.32	120.30
2	E	229	ARG	NE-CZ-NH1	7.96	124.28	120.30
1	C	362	ARG	NE-CZ-NH2	7.95	124.28	120.30
2	D	125	GLU	OE1-CD-OE2	-7.94	113.77	123.30
1	B	304	ARG	NE-CZ-NH2	7.88	124.24	120.30
1	B	219	ARG	NE-CZ-NH1	-7.74	116.43	120.30
1	C	450	ARG	NE-CZ-NH1	7.67	124.14	120.30
1	B	279	ARG	NE-CZ-NH2	-7.50	116.55	120.30
2	F	408	ARG	NE-CZ-NH2	7.40	124.00	120.30
1	B	270	ASP	CB-CA-C	-7.40	95.60	110.40
1	C	304	ARG	NE-CZ-NH2	7.36	123.98	120.30
1	A	450	ARG	NE-CZ-NH1	7.24	123.92	120.30
2	E	41	ARG	CD-NE-CZ	7.17	133.64	123.60
1	B	258	ARG	CD-NE-CZ	7.16	133.62	123.60
1	A	270	ASP	CB-CA-C	-7.10	96.19	110.40
2	F	139	VAL	CB-CA-C	-7.05	98.01	111.40
2	D	93	ARG	NE-CZ-NH1	-7.04	116.78	120.30
1	C	161	ARG	NE-CZ-NH2	-7.04	116.78	120.30
2	E	356	ARG	NE-CZ-NH2	-6.98	116.81	120.30
1	C	45	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	B	279	ARG	CD-NE-CZ	6.94	133.32	123.60
2	E	356	ARG	NE-CZ-NH1	6.93	123.77	120.30
3	G	77	LEU	CA-CB-CG	6.92	131.22	115.30
2	F	95	MET	C-N-CA	6.77	138.62	121.70
2	D	96	ASN	CB-CA-C	-6.66	97.09	110.40
1	B	349	GLN	CA-CB-CG	6.64	128.00	113.40
2	D	95	MET	C-N-CA	6.63	138.28	121.70
2	F	189	ARG	NE-CZ-NH2	6.60	123.60	120.30
1	C	308	ARG	NE-CZ-NH1	-6.56	117.02	120.30
2	D	274	ARG	NE-CZ-NH1	-6.55	117.02	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	59	ARG	NE-CZ-NH1	-6.55	117.03	120.30
1	B	423	ARG	CD-NE-CZ	6.54	132.76	123.60
1	A	106	ARG	CD-NE-CZ	6.52	132.73	123.60
2	D	231	ARG	NE-CZ-NH1	6.52	123.56	120.30
2	F	256	ASP	CB-CG-OD1	6.51	124.16	118.30
2	E	44	ARG	NE-CZ-NH2	-6.49	117.06	120.30
1	A	127	ARG	NE-CZ-NH2	-6.45	117.08	120.30
1	A	372	SER	N-CA-CB	6.43	120.15	110.50
1	A	371	VAL	CB-CA-C	-6.41	99.21	111.40
2	E	431	LEU	CA-CB-CG	6.40	130.01	115.30
1	B	270	ASP	CB-CG-OD1	6.39	124.05	118.30
2	D	191	ARG	NE-CZ-NH1	-6.33	117.14	120.30
2	F	12	ARG	NE-CZ-NH2	-6.33	117.14	120.30
1	A	170	ASP	CB-CG-OD1	6.29	123.96	118.30
1	A	398	ARG	NE-CZ-NH2	6.28	123.44	120.30
1	C	291	ARG	NE-CZ-NH1	6.28	123.44	120.30
2	D	372	ARG	NE-CZ-NH2	6.27	123.44	120.30
1	A	210	ARG	NE-CZ-NH2	-6.25	117.17	120.30
1	C	308	ARG	NE-CZ-NH2	6.25	123.43	120.30
1	A	171	ARG	NE-CZ-NH2	6.23	123.42	120.30
1	B	300	TYR	CB-CG-CD2	-6.21	117.28	121.00
2	E	274	ARG	NE-CZ-NH2	-6.19	117.20	120.30
1	C	476	HIS	N-CA-C	6.15	127.61	111.00
1	C	381	ARG	CD-NE-CZ	6.14	132.20	123.60
1	B	128	ARG	NE-CZ-NH1	6.13	123.37	120.30
2	F	97	VAL	CB-CA-C	-6.12	99.77	111.40
1	B	371	VAL	CB-CA-C	-6.12	99.77	111.40
1	B	127	ARG	CD-NE-CZ	6.12	132.16	123.60
1	C	423	ARG	CD-NE-CZ	6.09	132.13	123.60
1	C	164	ARG	CD-NE-CZ	-5.96	115.25	123.60
2	D	222	MET	CB-CA-C	-5.93	98.54	110.40
1	A	269	ASP	C-N-CA	5.89	136.43	121.70
1	B	139	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	B	337	TYR	CB-CG-CD1	5.73	124.44	121.00
1	A	40	ARG	NE-CZ-NH2	5.71	123.15	120.30
2	F	103	ASP	CB-CG-OD2	-5.71	113.17	118.30
1	A	297	ASP	CB-CG-OD2	-5.70	113.17	118.30
1	A	297	ASP	CB-CG-OD1	5.70	123.43	118.30
1	B	398	ARG	NE-CZ-NH1	-5.69	117.45	120.30
2	F	191	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	A	219	ARG	CD-NE-CZ	5.66	131.52	123.60
3	G	9	ARG	NE-CZ-NH1	5.65	123.13	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	41	ARG	CG-CD-NE	5.65	123.66	111.80
2	D	139	VAL	CB-CA-C	-5.65	100.67	111.40
1	B	210	ARG	NE-CZ-NH1	-5.63	117.49	120.30
2	D	474	ALA	C-N-CA	5.61	135.72	121.70
3	G	237	LYS	CB-CA-C	5.61	121.61	110.40
1	A	233	SER	N-CA-CB	-5.59	102.11	110.50
2	D	454	GLU	CA-CB-CG	5.55	125.61	113.40
2	D	431	LEU	CA-CB-CG	5.54	128.04	115.30
1	B	143	ARG	NE-CZ-NH2	5.50	123.05	120.30
2	D	12	ARG	NE-CZ-NH2	-5.49	117.56	120.30
2	D	372	ARG	NE-CZ-NH1	-5.48	117.56	120.30
1	B	423	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	B	349	GLN	N-CA-CB	5.47	120.45	110.60
2	E	93	ARG	NE-CZ-NH1	-5.46	117.57	120.30
1	A	335	SER	CB-CA-C	-5.43	99.77	110.10
1	C	170	ASP	CB-CG-OD1	5.40	123.16	118.30
1	B	222	ASP	CB-CG-OD2	-5.40	113.44	118.30
2	F	191	ARG	CD-NE-CZ	5.38	131.13	123.60
1	C	241	PRO	N-CA-CB	5.37	109.75	103.30
1	A	304	ARG	NE-CZ-NH1	-5.35	117.63	120.30
2	F	71	ARG	NE-CZ-NH2	5.35	122.97	120.30
1	C	349	GLN	CB-CA-C	-5.34	99.71	110.40
1	B	278	TYR	CB-CG-CD1	-5.29	117.83	121.00
1	B	45	ARG	CB-CG-CD	-5.28	97.86	111.60
2	E	260	ARG	NE-CZ-NH2	5.27	122.93	120.30
1	C	171	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	B	188	ARG	CG-CD-NE	5.23	122.79	111.80
2	F	100	GLU	OE1-CD-OE2	5.22	129.56	123.30
2	E	231	ARG	NE-CZ-NH1	-5.21	117.69	120.30
1	B	40	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	B	351	PHE	N-CA-CB	5.17	119.91	110.60
2	D	400	ASP	CB-CG-OD1	5.17	122.95	118.30
1	C	336	ALA	N-CA-CB	-5.17	102.86	110.10
2	E	408	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	A	270	ASP	CB-CG-OD1	5.16	122.95	118.30
1	A	258	ARG	CD-NE-CZ	5.13	130.78	123.60
2	D	316	ASP	CB-CG-OD2	-5.12	113.69	118.30
2	F	423	VAL	CB-CA-C	-5.11	101.68	111.40
2	E	122	GLU	CA-CB-CG	5.10	124.62	113.40
1	A	161	ARG	NE-CZ-NH2	-5.09	117.76	120.30
2	F	406	ARG	NE-CZ-NH1	-5.09	117.76	120.30
2	F	337	ARG	CD-NE-CZ	5.08	130.71	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	232	VAL	CB-CA-C	-5.07	101.76	111.40
2	E	223	ASN	CB-CA-C	-5.07	100.27	110.40
1	A	128	ARG	NE-CZ-NH1	-5.05	117.77	120.30
1	A	40	ARG	CG-CD-NE	5.05	122.40	111.80
2	D	356	ARG	CD-NE-CZ	-5.04	116.54	123.60
2	F	303	SER	N-CA-CB	-5.04	102.94	110.50
3	G	44	TYR	CA-CB-CG	5.04	122.97	113.40
2	E	96	ASN	N-CA-CB	-5.03	101.54	110.60
1	C	127	ARG	NH1-CZ-NH2	5.03	124.93	119.40
1	B	171	ARG	NE-CZ-NH2	-5.03	117.79	120.30
1	B	234	ALA	N-CA-C	-5.03	97.43	111.00
2	F	210	ASP	CB-CA-C	-5.03	100.35	110.40
1	B	300	TYR	CB-CG-CD1	5.02	124.01	121.00
1	A	452	TYR	CB-CG-CD1	-5.02	117.99	121.00
2	F	315	ASP	CB-CG-OD1	5.02	122.81	118.30
1	A	200	TYR	CA-CB-CG	-5.01	103.88	113.40
1	C	161	ARG	CD-NE-CZ	5.01	130.61	123.60

There are no chirality outliers.

There are no planarity outliers.

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	3715	0	3813	179	0
1	B	3656	0	3764	168	0
1	C	3748	0	3843	155	0
2	D	3539	0	3593	168	0
2	E	3530	0	3587	222	0
2	F	3530	0	3587	121	0
3	G	945	0	1019	60	0
All	All	22663	0	23206	972	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 21.

All (972) 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:B:283:LEU:CD1	2:E:277:SER:HB3	1.66	1.25
1:B:283:LEU:HD12	2:E:277:SER:HB3	1.13	1.11
1:C:127:ARG:HH12	1:C:255:GLU:HB2	1.00	1.08
3:G:39:LYS:HB2	3:G:40:PRO:HD3	1.35	1.05
1:C:215:GLN:HG3	2:F:356:ARG:HH22	1.18	1.03
2:F:275:ILE:HD13	3:G:271:ALA:CB	1.86	1.03
2:F:275:ILE:HD13	3:G:271:ALA:HB1	1.45	0.98
1:B:283:LEU:CD1	2:E:277:SER:CB	2.41	0.97
2:E:223:ASN:H	2:E:223:ASN:HD22	1.00	0.95
2:F:223:ASN:HD22	2:F:223:ASN:H	1.07	0.94
1:C:404:ALA:C	1:C:406:PHE:H	1.64	0.93
1:B:179:ALA:HB1	1:B:267:ILE:HD13	1.48	0.92
1:C:180:ILE:HD11	1:C:216:LEU:HD21	1.52	0.92
1:C:127:ARG:NH1	1:C:255:GLU:HB2	1.84	0.91
1:C:30:ARG:HE	1:C:87:ILE:HD11	1.37	0.89
2:E:89:GLU:HG2	2:E:110:THR:HG22	1.55	0.88
1:C:48:GLN:HB3	2:D:68:GLY:HA2	1.54	0.87
1:B:215:GLN:HE22	2:E:130:GLN:NE2	1.71	0.87
2:F:275:ILE:CD1	3:G:271:ALA:HB1	2.04	0.87
1:A:215:GLN:HG3	2:D:356:ARG:HH12	1.39	0.86
1:B:215:GLN:NE2	2:E:130:GLN:NE2	2.24	0.85
2:F:275:ILE:HD13	3:G:271:ALA:HB2	1.60	0.84
1:A:211:SER:HA	2:D:126:MET:HE2	1.59	0.83
2:E:223:ASN:H	2:E:223:ASN:ND2	1.72	0.83
1:A:400:VAL:HG12	1:A:418:LEU:HD21	1.60	0.83
1:B:456:LEU:HD12	1:B:457:GLU:H	1.43	0.83
2:E:316:ASP:OD2	3:G:254:ARG:NH1	2.12	0.82
1:B:209:LYS:HZ3	2:E:356:ARG:NH1	1.78	0.81
2:E:132:ILE:HD12	2:E:145:PRO:HB3	1.61	0.81
1:C:215:GLN:HG3	2:F:356:ARG:NH2	1.95	0.81
1:B:141:SER:O	1:B:143:ARG:HD2	1.83	0.79
2:D:136:GLY:HA3	2:D:431:LEU:HD13	1.65	0.78
1:B:186:GLN:HG3	1:B:199:LEU:HB3	1.65	0.78
2:D:282:GLN:H	2:D:282:GLN:HE21	1.30	0.78
1:A:215:GLN:HG3	2:D:356:ARG:NH1	1.98	0.78
1:C:399:GLU:OE2	2:D:408:ARG:NH2	2.17	0.78
2:E:370:VAL:HG21	2:E:438:ILE:HG22	1.65	0.77
1:A:211:SER:CA	2:D:126:MET:HE2	2.14	0.77
2:D:139:VAL:HG13	2:D:414:LEU:HD22	1.65	0.77
2:D:404:VAL:O	2:D:408:ARG:HG3	1.84	0.77
1:B:36:ASP:OD1	2:E:274:ARG:NE	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:130:GLN:HB3	2:F:357:ILE:HD11	1.67	0.76
1:A:392:LEU:HG	1:A:396:GLN:HE21	1.50	0.76
1:B:379:GLN:HB3	1:B:384:LYS:HE2	1.68	0.76
2:D:53:LEU:HD12	2:D:57:THR:HG22	1.66	0.76
3:G:2:THR:HG22	3:G:4:LYS:H	1.51	0.75
2:E:89:GLU:HG3	2:E:109:LYS:O	1.87	0.74
2:D:433:PRO:HG2	2:D:436:GLU:HG2	1.70	0.74
1:A:347:ASP:OD1	2:E:191:ARG:NH1	2.20	0.74
2:D:223:ASN:H	2:D:223:ASN:HD22	1.35	0.73
2:E:96:ASN:HB3	2:E:100:GLU:H	1.52	0.73
1:B:283:LEU:HD11	2:E:277:SER:CB	2.18	0.73
2:F:89:GLU:HG3	2:F:109:LYS:O	1.89	0.72
2:E:390:ILE:HG22	2:E:391:LEU:HD23	1.70	0.72
2:E:139:VAL:HG13	2:E:414:LEU:HD22	1.71	0.72
2:E:394:ASP:C	2:E:396:LEU:H	1.93	0.71
1:B:180:ILE:HD11	1:B:216:LEU:HD21	1.71	0.71
2:F:395:GLU:OE2	3:G:77:LEU:HA	1.90	0.71
2:E:38:VAL:HG21	2:E:45:LEU:HD23	1.71	0.71
2:D:84:ILE:HB	2:D:95:MET:HE3	1.73	0.71
2:E:183:PHE:HB3	2:E:217:LEU:HD22	1.72	0.70
1:C:211:SER:O	1:C:215:GLN:HG2	1.92	0.70
2:D:96:ASN:HB2	2:D:100:GLU:H	1.56	0.70
1:A:479:LEU:HA	1:A:482:LYS:HE3	1.73	0.70
1:C:34:ILE:HD11	1:C:79:ASP:HB2	1.72	0.70
2:E:388:ILE:HG23	2:E:393:MET:HG3	1.72	0.70
1:A:97:VAL:HA	1:A:126:ARG:HH21	1.56	0.70
1:B:452:TYR:OH	1:B:498:LYS:HG3	1.92	0.70
2:E:391:LEU:HD21	3:G:28:ALA:HB3	1.74	0.70
1:A:407:GLY:HA2	1:A:410:LEU:HD21	1.74	0.69
2:E:321:ALA:HB3	2:E:322:PRO:HD3	1.75	0.69
1:B:209:LYS:NZ	2:E:356:ARG:NH1	2.39	0.69
1:A:211:SER:N	2:D:126:MET:HE1	2.06	0.69
2:F:223:ASN:N	2:F:223:ASN:HD22	1.85	0.69
2:F:275:ILE:CD1	3:G:271:ALA:CB	2.65	0.69
1:B:209:LYS:HZ3	2:E:356:ARG:HH12	1.39	0.69
1:A:137:ILE:HG13	2:E:104:GLU:HG3	1.74	0.69
2:E:105:ARG:CZ	2:E:208:LEU:HD23	2.23	0.69
2:F:89:GLU:HG2	2:F:110:THR:HG22	1.75	0.68
1:A:215:GLN:NE2	2:D:128:VAL:HA	2.08	0.68
1:C:385:GLN:OE1	1:C:488:LYS:HG2	1.93	0.68
2:D:393:MET:HE3	2:D:404:VAL:HG21	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:433:PRO:HD2	2:E:436:GLU:HB2	1.74	0.68
1:C:418:LEU:O	1:C:422:VAL:HG23	1.94	0.68
2:E:313:PRO:HD2	2:E:322:PRO:HG3	1.76	0.68
2:F:252:LEU:HD23	2:F:305:THR:HB	1.75	0.68
1:A:440:GLU:O	1:A:444:VAL:HG13	1.94	0.67
2:F:409:LYS:HD3	2:F:457:PHE:CE2	2.30	0.67
2:E:345:TYR:HA	2:E:346:PRO:C	2.13	0.67
1:A:44:LEU:O	1:A:47:VAL:HG22	1.94	0.67
1:B:156:LEU:HD22	1:B:391:LYS:HD2	1.77	0.67
2:E:136:GLY:HA3	2:E:431:LEU:HD13	1.77	0.67
3:G:39:LYS:CB	3:G:40:PRO:HD3	2.15	0.67
1:C:59:LEU:HD23	1:C:82:ILE:HD11	1.77	0.67
2:D:223:ASN:N	2:D:223:ASN:HD22	1.89	0.66
2:F:223:ASN:ND2	2:F:223:ASN:H	1.85	0.66
1:A:376:SER:HB3	1:A:384:LYS:HE2	1.78	0.66
1:C:173:THR:HG22	1:C:354:THR:HG22	1.77	0.66
2:F:314:ALA:O	2:F:315:ASP:HB2	1.95	0.66
1:A:134:PRO:O	1:A:139:ARG:NH2	2.27	0.66
1:B:283:LEU:HD12	2:E:277:SER:CB	2.06	0.66
2:E:359:ASP:OD2	2:E:361:ASN:HB2	1.96	0.66
2:F:344:ILE:HG23	2:F:415:SER:HB3	1.78	0.66
1:A:97:VAL:HB	1:A:98:PRO:HD2	1.76	0.65
3:G:24:LYS:HE3	3:G:233:ASP:HB2	1.78	0.65
2:F:80:ALA:HB1	2:F:81:PRO:CD	2.25	0.65
2:D:54:GLY:O	2:D:55:GLU:HB2	1.96	0.65
2:F:200:MET:HG3	2:F:205:VAL:CG2	2.27	0.65
1:B:44:LEU:HB3	1:B:47:VAL:HG22	1.77	0.65
1:C:44:LEU:O	1:C:47:VAL:HG22	1.97	0.65
2:D:223:ASN:ND2	2:D:223:ASN:H	1.93	0.65
1:B:83:LYS:HD3	2:E:31:PRO:HB3	1.78	0.65
2:F:136:GLY:HA3	2:F:431:LEU:CD1	2.26	0.65
2:D:167:MET:HB3	2:D:420:VAL:HG11	1.78	0.65
1:B:333:ASP:HB2	3:G:252:ARG:HH21	1.62	0.64
1:C:289:PRO:HD2	3:G:268:GLY:HA2	1.79	0.64
2:F:200:MET:HG3	2:F:205:VAL:HG23	1.80	0.64
1:A:471:HIS:CE1	1:A:475:GLN:HG3	2.32	0.64
1:C:188:ARG:HH21	1:C:437:ALA:HB2	1.62	0.64
1:A:107:VAL:HG11	2:D:123:PHE:CE2	2.32	0.64
2:F:94:ILE:HG22	2:F:102:ILE:HD11	1.80	0.64
1:C:99:VAL:HG22	1:C:253:MET:HA	1.78	0.64
1:C:202:ILE:HG12	1:C:230:ILE:HD12	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:419:SER:O	1:C:423:ARG:HG2	1.98	0.64
2:D:200:MET:HB3	2:D:206:ILE:HG13	1.79	0.64
2:F:136:GLY:HA3	2:F:431:LEU:HD12	1.80	0.64
1:C:404:ALA:C	1:C:406:PHE:N	2.44	0.63
2:E:346:PRO:HG3	2:E:418:PHE:CZ	2.33	0.63
2:E:425:THR:O	2:E:427:HIS:ND1	2.20	0.63
2:E:443:GLN:HG2	2:E:448:GLU:OE2	1.98	0.63
1:B:188:ARG:HH21	1:B:437:ALA:HB2	1.62	0.63
1:C:488:LYS:HG2	1:C:489:ILE:H	1.63	0.63
1:B:389:THR:HA	1:B:392:LEU:CD1	2.28	0.63
2:E:298:THR:HG23	2:E:303:SER:HB3	1.81	0.63
2:F:363:VAL:HG23	2:F:367:HIS:HB3	1.81	0.63
2:E:223:ASN:HD22	2:E:223:ASN:N	1.84	0.62
2:E:139:VAL:CG1	2:E:414:LEU:HD22	2.28	0.62
2:E:400:ASP:O	2:E:404:VAL:HG23	1.98	0.62
2:E:204:GLY:O	2:E:206:ILE:N	2.32	0.62
2:F:87:GLY:HA2	2:F:242:TYR:CE2	2.35	0.62
1:A:341:ASN:O	1:A:345:ILE:HG13	1.99	0.62
1:C:52:MET:O	1:C:91:THR:HB	1.99	0.62
1:B:397:TYR:CD1	1:B:421:GLY:HA3	2.34	0.62
1:C:151:LYS:HE3	1:C:430:GLN:HG3	1.82	0.62
1:B:184:ILE:HG22	1:B:435:PRO:HG2	1.81	0.62
2:E:138:LYS:HE2	2:E:432:VAL:HG21	1.80	0.62
1:B:36:ASP:OD1	2:E:274:ARG:CZ	2.48	0.62
1:C:292:GLU:O	1:C:293:ALA:HB3	2.00	0.62
2:D:396:LEU:HD22	2:D:400:ASP:CB	2.30	0.62
2:E:422:GLU:HG2	2:E:427:HIS:O	1.99	0.62
1:A:45:ARG:HH11	1:A:45:ARG:HG2	1.64	0.61
2:E:394:ASP:C	2:E:396:LEU:N	2.54	0.61
2:E:201:ILE:HD13	2:E:208:LEU:HD11	1.82	0.61
1:A:439:GLU:HG2	1:A:484:ARG:HB2	1.83	0.61
1:A:270:ASP:OD1	1:A:273:LYS:HG3	2.01	0.61
1:B:102:GLU:HG3	1:B:122:GLY:O	2.00	0.61
1:B:389:THR:HA	1:B:392:LEU:HD12	1.81	0.61
1:B:422:VAL:O	1:B:426:GLU:HG2	2.00	0.61
1:A:121:ILE:HD13	1:A:121:ILE:H	1.66	0.60
1:A:283:LEU:HD21	1:A:289:PRO:HB3	1.83	0.60
1:A:394:LEU:HD11	1:A:428:LEU:HD11	1.82	0.60
1:B:437:ALA:O	1:B:440:GLU:N	2.30	0.60
1:B:479:LEU:HD11	1:B:497:LEU:HD13	1.83	0.60
1:C:362:ARG:HA	1:C:363:PRO:C	2.21	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:89:GLU:HG2	2:D:110:THR:HG22	1.83	0.60
1:A:40:ARG:HG3	1:A:40:ARG:HH11	1.66	0.60
2:E:149:GLY:HA2	2:E:304:ILE:O	2.02	0.60
1:B:51:GLU:HA	1:B:94:ILE:HA	1.83	0.60
2:D:93:ARG:HH11	2:D:93:ARG:HG3	1.66	0.60
2:E:32:ILE:O	2:E:33:LEU:HB2	2.02	0.60
2:E:397:SER:H	2:E:400:ASP:HB2	1.66	0.60
1:A:157:VAL:N	1:A:158:PRO:CD	2.65	0.60
1:A:376:SER:C	1:A:378:ALA:H	2.03	0.60
1:C:313:ASN:OD1	1:C:316:PHE:HD1	1.85	0.60
1:A:211:SER:CA	2:D:126:MET:CE	2.79	0.60
3:G:239:ALA:O	3:G:243:ILE:HG13	2.02	0.60
1:A:52:MET:O	1:A:91:THR:HG23	2.02	0.60
1:C:99:VAL:HG13	1:C:256:TYR:HB2	1.83	0.60
2:E:226:PRO:HB3	2:E:267:GLU:HB2	1.84	0.60
1:A:166:LEU:HA	1:A:325:PRO:HD2	1.83	0.60
1:C:136:ILE:O	2:D:194:ASN:OD1	2.19	0.60
1:C:407:GLY:HA2	1:C:410:LEU:HD11	1.84	0.60
1:A:211:SER:N	2:D:126:MET:CE	2.64	0.60
2:F:122:GLU:HB2	2:F:125:GLU:HG3	1.84	0.60
1:B:397:TYR:CG	1:B:421:GLY:HA3	2.37	0.59
1:A:457:GLU:CB	1:A:460:LYS:HD3	2.32	0.59
1:B:362:ARG:HA	1:B:363:PRO:C	2.22	0.59
2:E:200:MET:HB3	2:E:205:VAL:HG23	1.84	0.59
1:A:376:SER:C	1:A:378:ALA:N	2.55	0.59
1:A:432:GLN:HB3	1:A:433:TYR:CD2	2.37	0.59
2:D:317:LEU:HD22	2:D:326:PHE:HZ	1.67	0.59
2:E:419:GLN:HG3	2:E:429:GLY:HA3	1.84	0.59
3:G:39:LYS:HB2	3:G:40:PRO:CD	2.24	0.59
2:D:263:GLN:O	2:D:267:GLU:HG3	2.03	0.59
1:B:499:GLU:O	1:B:502:THR:HB	2.03	0.59
2:E:223:ASN:ND2	2:E:223:ASN:N	2.46	0.59
2:E:408:ARG:O	2:E:412:ARG:HG3	2.03	0.59
1:C:406:PHE:O	1:C:408:SER:N	2.36	0.59
2:F:29:LEU:HD12	2:F:30:PRO:HD2	1.85	0.59
1:B:391:LYS:O	1:B:395:ALA:N	2.36	0.59
1:B:411:ASP:HB3	1:B:414:THR:OG1	2.02	0.59
1:B:434:SER:N	1:B:435:PRO:HD3	2.18	0.59
1:B:438:ILE:O	1:B:442:VAL:HG22	2.02	0.58
1:B:452:TYR:O	1:B:453:LEU:HD23	2.03	0.58
1:C:102:GLU:OE2	1:C:123:SER:HA	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:ILE:HD11	1:C:143:ARG:NH2	2.18	0.58
2:D:186:VAL:HG13	2:D:232:VAL:HG23	1.85	0.58
3:G:13:ILE:HG22	3:G:243:ILE:HG12	1.84	0.58
1:A:472:VAL:HG23	1:A:480:LEU:HD11	1.85	0.58
1:C:464:PHE:CE1	1:C:505:LEU:HD23	2.39	0.58
1:B:400:VAL:HB	1:B:418:LEU:HD21	1.85	0.58
2:F:105:ARG:NH1	2:F:208:LEU:HD23	2.18	0.58
1:B:170:ASP:O	1:B:175:LYS:HE2	2.03	0.58
1:B:34:ILE:HG23	2:E:32:ILE:HD11	1.85	0.58
2:E:95:MET:CG	2:E:99:GLY:HA2	2.34	0.58
2:E:391:LEU:HD21	3:G:28:ALA:CB	2.32	0.58
1:B:286:ARG:NH2	2:E:273:GLY:O	2.36	0.58
1:B:83:LYS:HD2	2:E:31:PRO:HA	1.85	0.58
1:A:373:ARG:HD3	2:E:192:GLU:OE2	2.04	0.58
1:B:352:LEU:HA	1:B:364:ALA:O	2.04	0.58
1:B:80:LYS:HE3	2:E:119:GLU:OE2	2.03	0.58
1:A:180:ILE:HD11	1:A:216:LEU:HD21	1.86	0.57
1:A:219:ARG:HH11	1:A:219:ARG:HB2	1.69	0.57
1:C:374:VAL:HG11	1:C:378:ALA:HB2	1.85	0.57
2:D:473:LEU:C	2:D:475:GLU:H	2.08	0.57
1:C:78:ASN:ND2	1:C:80:LYS:HD3	2.19	0.57
1:C:218:LYS:HD2	2:F:128:VAL:HG21	1.85	0.57
3:G:17:GLN:HB2	3:G:239:ALA:HB1	1.85	0.57
1:A:209:LYS:HB2	2:D:294:GLU:OE1	2.04	0.57
2:E:138:LYS:O	2:E:142:LEU:HB3	2.04	0.57
2:F:96:ASN:HD22	2:F:100:GLU:HB2	1.68	0.57
2:E:246:GLN:NE2	2:E:246:GLN:HA	2.19	0.57
2:E:267:GLU:O	2:E:271:LEU:HG	2.05	0.57
1:C:107:VAL:HG12	1:C:115:ILE:HD11	1.86	0.57
2:D:237:LEU:HD13	2:D:296:ILE:HG12	1.85	0.57
2:E:105:ARG:NH2	2:E:208:LEU:HA	2.20	0.57
1:B:357:PHE:CE1	1:B:362:ARG:HD3	2.40	0.57
1:B:51:GLU:OE2	1:B:90:ARG:HB3	2.05	0.57
1:C:173:THR:CG2	1:C:354:THR:HG22	2.35	0.57
2:F:440:GLY:O	2:F:444:ILE:HG13	2.04	0.57
1:A:185:ASN:O	1:A:188:ARG:HG3	2.05	0.57
1:C:187:LYS:HE2	1:C:191:ASP:OD2	2.05	0.57
1:C:292:GLU:HA	3:G:264:GLU:OE2	2.05	0.57
1:C:156:LEU:HD13	1:C:367:VAL:HG22	1.86	0.56
2:E:122:GLU:N	2:E:125:GLU:OE2	2.37	0.56
2:E:158:ALA:C	2:E:160:VAL:H	2.08	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:155:PHE:CE1	2:E:310:ILE:HD12	2.40	0.56
2:F:324:THR:O	2:F:324:THR:HG22	2.05	0.56
2:F:32:ILE:O	2:F:33:LEU:HB2	2.05	0.56
1:A:450:ARG:NH2	1:A:494:ASP:OD2	2.38	0.56
1:B:351:PHE:CE1	1:B:369:LEU:HB3	2.41	0.56
1:C:184:ILE:HG22	1:C:435:PRO:HG2	1.87	0.56
1:C:408:SER:O	1:C:409:ASP:C	2.44	0.56
3:G:20:THR:HG21	3:G:236:SER:N	2.20	0.56
2:E:433:PRO:HG2	2:E:436:GLU:HG2	1.86	0.56
2:E:224:GLU:O	2:E:229:ARG:NH1	2.32	0.56
2:E:174:ALA:CB	2:E:214:LYS:HD3	2.36	0.56
1:A:159:ILE:HD12	1:A:165:GLU:HG2	1.88	0.56
1:C:399:GLU:CD	2:D:408:ARG:HH22	2.09	0.56
2:D:366:GLU:HG3	2:D:442:GLN:HE22	1.71	0.56
2:F:10:THR:HG23	2:F:76:LEU:HD12	1.88	0.56
1:B:393:GLU:OE1	1:B:424:LEU:HD11	2.05	0.56
2:E:138:LYS:HG3	2:E:416:GLN:OE1	2.06	0.56
1:C:394:LEU:HD22	1:C:398:ARG:HH21	1.71	0.55
1:C:48:GLN:HB3	2:D:68:GLY:CA	2.33	0.55
2:D:255:ILE:HG21	2:D:258:ILE:HD13	1.87	0.55
2:E:397:SER:C	2:E:399:GLU:N	2.57	0.55
1:A:99:VAL:CG2	1:A:253:MET:HA	2.37	0.55
2:E:92:GLY:N	2:E:215:VAL:O	2.30	0.55
1:A:107:VAL:HG12	1:A:115:ILE:HD11	1.87	0.55
1:C:219:ARG:HD3	1:C:433:TYR:CE1	2.41	0.55
1:C:442:VAL:CG1	1:C:489:ILE:HD11	2.37	0.55
2:D:87:GLY:HA2	2:D:242:TYR:CE2	2.42	0.55
2:D:451:HIS:CD2	2:D:452:LEU:HD23	2.42	0.55
2:E:263:GLN:O	2:E:267:GLU:HG3	2.07	0.55
2:F:14:VAL:O	2:F:71:ARG:HG2	2.05	0.55
1:C:102:GLU:HG2	1:C:122:GLY:O	2.06	0.55
1:C:404:ALA:O	1:C:406:PHE:N	2.37	0.55
1:B:482:LYS:O	1:B:486:ASP:N	2.37	0.55
1:C:433:TYR:C	1:C:435:PRO:HD3	2.26	0.55
1:C:52:MET:HG3	1:C:61:GLY:O	2.07	0.55
2:D:83:ARG:HA	2:D:114:ALA:O	2.07	0.55
1:B:270:ASP:OD1	1:B:273:LYS:HG3	2.07	0.55
1:B:423:ARG:HE	1:B:458:PRO:HD3	1.72	0.55
1:B:423:ARG:HE	1:B:458:PRO:HG3	1.71	0.55
2:D:142:LEU:HD22	2:D:441:PHE:CD2	2.42	0.55
2:D:471:ASP:O	2:D:474:ALA:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:98:ILE:HG13	2:F:100:GLU:HG3	1.88	0.55
1:A:209:LYS:HE3	1:A:211:SER:HB2	1.88	0.54
1:B:80:LYS:HG3	1:B:81:LEU:HD23	1.88	0.54
2:E:244:ARG:HG3	2:E:303:SER:N	2.22	0.54
2:E:77:ASP:OD1	2:E:79:GLY:N	2.34	0.54
1:B:441:GLN:O	1:B:445:ILE:HG12	2.08	0.54
2:E:397:SER:O	2:E:401:LYS:HG3	2.08	0.54
1:C:283:LEU:HD21	1:C:289:PRO:HB3	1.89	0.54
2:F:63:MET:CE	2:F:97:VAL:HG11	2.36	0.54
1:A:452:TYR:OH	1:A:498:LYS:HG3	2.08	0.54
1:B:347:ASP:HB3	1:B:374:VAL:HG22	1.88	0.54
2:E:396:LEU:HB3	2:E:401:LYS:HG2	1.88	0.54
1:B:114:ALA:HB2	1:B:121:ILE:HD11	1.89	0.54
2:D:167:MET:CB	2:D:420:VAL:HG11	2.38	0.54
2:E:218:VAL:HG11	2:E:235:THR:CG2	2.38	0.54
1:A:479:LEU:HD21	1:A:493:SER:HB3	1.89	0.54
2:D:473:LEU:O	2:D:475:GLU:N	2.40	0.54
2:E:174:ALA:HB2	2:E:214:LYS:HD3	1.90	0.54
1:C:239:ALA:HB1	1:C:241:PRO:HD2	1.90	0.54
2:D:412:ARG:HG3	2:D:412:ARG:HH11	1.73	0.54
1:A:170:ASP:O	1:A:175:LYS:HE2	2.08	0.54
1:A:373:ARG:HG3	1:A:373:ARG:HH11	1.72	0.54
1:C:91:THR:HG22	1:C:93:ALA:H	1.72	0.54
2:D:388:ILE:HD12	2:D:393:MET:SD	2.48	0.54
1:A:150:ILE:HA	1:A:430:GLN:OE1	2.08	0.54
3:G:81:ILE:HG22	3:G:82:HIS:HD2	1.73	0.54
1:B:180:ILE:O	1:B:181:ASP:C	2.47	0.54
2:D:396:LEU:HD22	2:D:400:ASP:HB3	1.89	0.54
2:E:201:ILE:CD1	2:E:208:LEU:HD11	2.37	0.54
1:B:446:TYR:CD2	1:B:497:LEU:HD23	2.43	0.53
2:D:282:GLN:H	2:D:282:GLN:NE2	2.01	0.53
1:A:463:LYS:HD3	1:A:508:PHE:HZ	1.73	0.53
2:D:381:TYR:HE2	2:D:411:GLN:HE22	1.56	0.53
1:B:44:LEU:O	1:B:47:VAL:HG22	2.08	0.53
1:A:100:GLY:HA2	1:A:256:TYR:CE1	2.42	0.53
1:A:457:GLU:HB3	1:A:460:LYS:HD3	1.89	0.53
2:D:122:GLU:HA	2:D:122:GLU:OE1	2.07	0.53
2:F:292:MET:CE	2:F:296:ILE:HD11	2.38	0.53
2:F:439:LYS:HE3	2:F:443:GLN:HE22	1.73	0.53
1:A:207:GLY:HA3	1:A:273:LYS:HD3	1.90	0.53
1:C:215:GLN:HE22	2:F:128:VAL:HA	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:MET:HG3	1:A:441:GLN:HG2	1.90	0.53
1:B:69:ASP:O	1:B:70:ASN:HB3	2.09	0.53
1:C:210:ARG:NH1	2:F:121:PRO:O	2.42	0.53
2:D:31:PRO:HD2	2:D:34:ASN:ND2	2.24	0.53
2:D:412:ARG:HD2	2:D:454:GLU:HB3	1.90	0.53
2:D:136:GLY:CA	2:D:431:LEU:HD13	2.37	0.53
2:D:84:ILE:HD12	2:D:95:MET:HE1	1.90	0.53
1:B:283:LEU:HD11	2:E:277:SER:HB2	1.91	0.53
1:A:468:PHE:CE1	1:A:501:VAL:HG12	2.43	0.53
1:C:156:LEU:HD11	1:C:428:LEU:HD13	1.91	0.53
1:C:190:ASN:HA	1:C:198:LYS:HG2	1.91	0.53
1:C:270:ASP:OD1	1:C:273:LYS:HG3	2.09	0.53
2:F:210:ASP:HB2	2:F:212:THR:HG23	1.91	0.53
1:C:405:GLN:C	1:C:406:PHE:HD1	2.11	0.53
2:D:473:LEU:C	2:D:475:GLU:N	2.62	0.53
1:A:296:GLY:HA3	2:E:271:LEU:HD23	1.91	0.53
2:E:80:ALA:HB1	2:E:81:PRO:HD2	1.91	0.53
2:E:97:VAL:HG13	2:E:232:VAL:CG1	2.39	0.53
3:G:14:LYS:HG2	3:G:243:ILE:HD13	1.91	0.53
1:A:161:ARG:HH11	1:A:263:HIS:CG	2.25	0.52
1:B:358:TYR:C	1:B:360:GLY:H	2.12	0.52
1:C:436:MET:HE1	1:C:469:LEU:HD21	1.91	0.52
2:D:431:LEU:C	2:D:431:LEU:HD12	2.29	0.52
1:B:80:LYS:CE	2:E:119:GLU:OE2	2.57	0.52
2:E:334:VAL:HG23	2:E:353:SER:HA	1.92	0.52
2:F:96:ASN:HB2	2:F:100:GLU:H	1.74	0.52
3:G:37:GLU:OE1	3:G:218:LYS:HE3	2.10	0.52
1:C:180:ILE:CD1	1:C:216:LEU:HD21	2.34	0.52
2:E:220:GLY:HA3	2:E:232:VAL:HG21	1.91	0.52
2:E:218:VAL:HG11	2:E:235:THR:HG22	1.92	0.52
1:B:423:ARG:HD2	1:B:461:ILE:HD11	1.92	0.52
1:B:456:LEU:HD12	1:B:457:GLU:N	2.20	0.52
1:B:479:LEU:HA	1:B:482:LYS:HE3	1.90	0.52
1:B:140:ILE:HG23	1:B:311:LYS:HG3	1.92	0.52
2:E:254:PHE:CD1	2:E:307:VAL:HB	2.45	0.52
3:G:214:TYR:CZ	3:G:218:LYS:HG3	2.45	0.52
1:A:140:ILE:HG21	1:A:313:ASN:HA	1.92	0.52
2:D:422:GLU:HG2	2:D:427:HIS:O	2.09	0.52
2:E:81:PRO:HG2	2:E:115:ALA:HB1	1.91	0.52
3:G:17:GLN:HB2	3:G:239:ALA:CB	2.39	0.52
1:A:215:GLN:NE2	2:D:128:VAL:CA	2.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:157:VAL:N	1:B:158:PRO:HD3	2.25	0.52
1:B:386:VAL:HG22	1:B:442:VAL:HG12	1.91	0.52
1:C:267:ILE:N	1:C:267:ILE:HD12	2.25	0.52
2:E:84:ILE:HB	2:E:95:MET:HE1	1.92	0.52
2:D:96:ASN:CB	2:D:100:GLU:H	2.22	0.52
1:A:179:ALA:HB1	1:A:267:ILE:HG12	1.91	0.51
1:C:436:MET:CE	1:C:469:LEU:HD21	2.41	0.51
2:D:266:SER:HB3	2:D:282:GLN:HE22	1.75	0.51
2:E:377:ILE:HG21	2:E:410:ILE:CD1	2.40	0.51
2:E:9:THR:HG21	2:E:28:GLY:O	2.09	0.51
2:F:257:ASN:HB3	2:F:260:ARG:HG2	1.92	0.51
2:E:279:VAL:O	2:E:279:VAL:HG12	2.10	0.51
3:G:6:ILE:HG23	3:G:246:LEU:HD22	1.93	0.51
1:A:215:GLN:NE2	2:D:128:VAL:HG12	2.25	0.51
2:D:356:ARG:HG2	2:D:356:ARG:O	2.09	0.51
2:E:443:GLN:O	2:E:446:ALA:HB3	2.10	0.51
1:C:140:ILE:HD11	1:C:143:ARG:HH22	1.74	0.51
2:F:234:LEU:O	2:F:237:LEU:HB3	2.10	0.51
2:F:360:PRO:HD3	2:F:368:TYR:CD2	2.45	0.51
3:G:1:ALA:HB1	3:G:6:ILE:HD11	1.92	0.51
1:A:457:GLU:HB2	1:A:460:LYS:HD3	1.92	0.51
1:C:164:ARG:HD2	1:C:306:LEU:O	2.11	0.51
1:C:45:ARG:NH2	1:C:68:PRO:O	2.44	0.51
2:F:421:ALA:O	2:F:425:THR:HG23	2.11	0.51
2:E:25:PHE:O	2:E:56:SER:HB3	2.10	0.51
2:D:154:LEU:HD22	2:D:165:LEU:HD23	1.92	0.51
2:E:142:LEU:HD21	2:E:374:VAL:HG21	1.93	0.51
2:E:444:ILE:HD11	2:E:463:ILE:HD11	1.93	0.51
2:E:82:ILE:HB	2:E:116:ILE:HD13	1.92	0.51
1:A:67:GLU:O	2:E:71:ARG:NH1	2.39	0.51
1:B:157:VAL:N	1:B:158:PRO:CD	2.73	0.51
1:C:406:PHE:N	1:C:406:PHE:CD1	2.79	0.51
2:D:84:ILE:HD13	2:D:235:THR:HG23	1.92	0.51
2:E:321:ALA:HB3	2:E:322:PRO:CD	2.40	0.51
3:G:38:LEU:HD11	3:G:42:ARG:NE	2.26	0.51
2:D:366:GLU:CG	2:D:442:GLN:HE22	2.23	0.51
2:E:293:GLN:HG3	2:E:328:HIS:CG	2.46	0.51
2:F:96:ASN:ND2	2:F:100:GLU:HB2	2.26	0.51
1:B:386:VAL:CG2	1:B:442:VAL:HG12	2.41	0.50
1:C:443:ALA:O	1:C:446:TYR:HB3	2.10	0.50
2:E:382:LYS:O	2:E:385:GLN:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:ILE:HD11	1:A:143:ARG:NE	2.25	0.50
2:D:425:THR:HG21	2:D:459:MET:HE1	1.93	0.50
1:B:489:ILE:HG22	1:B:494:ASP:HB2	1.93	0.50
2:E:221:GLN:N	2:E:224:GLU:OE1	2.44	0.50
2:E:241:GLU:HA	2:E:304:ILE:HD11	1.94	0.50
1:A:187:LYS:HE2	1:A:191:ASP:OD2	2.11	0.50
1:A:294:TYR:HB2	1:A:337:TYR:HE2	1.76	0.50
1:B:390:MET:CE	1:B:428:LEU:HD21	2.42	0.50
1:C:64:LEU:HD23	1:C:74:VAL:HG21	1.92	0.50
2:D:406:ARG:O	2:D:410:ILE:HG13	2.11	0.50
2:E:155:PHE:HE1	2:E:310:ILE:HD12	1.77	0.50
1:A:347:ASP:OD1	2:E:191:ARG:HD3	2.10	0.50
2:F:242:TYR:CD1	2:F:246:GLN:HG3	2.46	0.50
3:G:30:LYS:HA	3:G:33:ARG:HE	1.76	0.50
1:A:224:ASP:CG	1:A:227:LYS:HE3	2.31	0.50
1:C:402:ALA:O	1:C:405:GLN:HG3	2.12	0.50
1:C:211:SER:HB3	2:F:126:MET:HE3	1.94	0.50
1:A:137:ILE:N	1:A:138:PRO:CD	2.75	0.50
1:A:380:THR:O	1:A:384:LYS:HG3	2.12	0.50
1:C:23:VAL:O	1:C:23:VAL:HG12	2.11	0.50
1:C:244:TYR:O	1:C:247:PRO:HD2	2.11	0.50
1:C:331:ALA:O	1:C:333:ASP:N	2.44	0.50
2:E:275:ILE:O	2:E:283:PRO:HG3	2.12	0.50
2:E:377:ILE:HG21	2:E:410:ILE:HD12	1.92	0.50
2:F:163:THR:O	2:F:167:MET:HG2	2.12	0.50
1:A:240:ALA:N	1:A:241:PRO:HD2	2.27	0.50
1:B:99:VAL:HG21	1:B:127:ARG:HB3	1.94	0.50
1:B:27:GLU:O	1:B:90:ARG:HG3	2.12	0.50
1:C:96:ASP:O	1:C:97:VAL:HG13	2.12	0.50
1:A:215:GLN:NE2	2:D:128:VAL:CB	2.75	0.50
2:D:168:GLU:O	2:D:168:GLU:HG3	2.11	0.50
3:G:82:HIS:CD2	3:G:82:HIS:H	2.29	0.50
1:C:434:SER:N	1:C:435:PRO:HD3	2.27	0.49
1:C:52:MET:HE3	1:C:95:VAL:HG13	1.92	0.49
2:E:462:PRO:HD2	2:E:465:GLU:HG3	1.94	0.49
1:C:225:ALA:HA	1:C:228:TYR:CE1	2.47	0.49
2:D:397:SER:O	2:D:400:ASP:N	2.45	0.49
2:E:463:ILE:O	2:E:467:VAL:HG23	2.12	0.49
1:B:151:LYS:NZ	1:B:429:LYS:O	2.45	0.49
2:F:386:ASP:O	2:F:389:ALA:HB3	2.12	0.49
1:B:300:TYR:O	1:B:304:ARG:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:168:GLU:OE1	2:F:418:PHE:HB3	2.12	0.49
1:B:49:ALA:O	1:B:50:GLU:HB2	2.12	0.49
2:D:136:GLY:HA2	2:D:432:VAL:O	2.12	0.49
2:D:417:PRO:HB3	2:D:459:MET:HE3	1.95	0.49
2:E:134:VAL:HG13	2:E:141:ASP:OD2	2.13	0.49
2:E:390:ILE:HG13	3:G:25:MET:HG2	1.95	0.49
3:G:210:ALA:HA	3:G:213:ILE:HB	1.93	0.49
2:D:83:ARG:HA	2:D:115:ALA:HA	1.95	0.49
2:F:339:ILE:HG22	2:F:344:ILE:HB	1.95	0.49
1:A:300:TYR:O	1:A:304:ARG:HG2	2.13	0.49
1:A:373:ARG:NH1	1:A:373:ARG:HG3	2.28	0.49
1:C:48:GLN:CB	2:D:68:GLY:HA2	2.36	0.49
1:B:107:VAL:HG12	1:B:115:ILE:CG1	2.42	0.49
1:B:423:ARG:HE	1:B:458:PRO:CD	2.26	0.49
1:A:296:GLY:HA3	2:E:271:LEU:CD2	2.42	0.48
1:B:96:ASP:HB2	1:B:127:ARG:O	2.12	0.48
1:B:427:LEU:HD11	1:B:448:GLY:HA3	1.95	0.48
1:C:334:VAL:HG13	1:C:351:PHE:CE1	2.48	0.48
2:D:93:ARG:NH1	2:D:93:ARG:HG3	2.27	0.48
1:A:94:ILE:HG12	1:A:95:VAL:N	2.27	0.48
1:B:351:PHE:HE1	1:B:369:LEU:O	1.96	0.48
2:F:86:VAL:HG11	2:F:114:ALA:HB3	1.94	0.48
3:G:20:THR:HG22	3:G:236:SER:HB3	1.94	0.48
1:C:335:SER:O	2:D:314:ALA:HA	2.13	0.48
1:A:389:THR:O	1:A:393:GLU:HG2	2.14	0.48
1:B:463:LYS:HE2	1:B:508:PHE:CZ	2.48	0.48
2:E:416:GLN:HG3	2:E:417:PRO:HD2	1.96	0.48
2:E:54:GLY:O	2:E:55:GLU:HB2	2.13	0.48
1:A:417:LEU:HD23	1:A:417:LEU:H	1.77	0.48
1:B:180:ILE:CD1	1:B:216:LEU:HD21	2.39	0.48
1:B:24:ASP:O	1:B:28:THR:HB	2.12	0.48
2:F:321:ALA:HB3	2:F:322:PRO:HD3	1.94	0.48
1:C:44:LEU:HB3	1:C:47:VAL:HG22	1.95	0.48
2:D:84:ILE:N	2:D:114:ALA:O	2.42	0.48
1:A:127:ARG:HE	1:A:131:LEU:CD1	2.27	0.48
1:A:313:ASN:O	1:A:316:PHE:N	2.37	0.48
1:C:362:ARG:HG3	1:C:362:ARG:NH1	2.27	0.48
2:E:227:GLY:O	2:E:230:ALA:HB3	2.13	0.48
2:E:444:ILE:HD11	2:E:463:ILE:CD1	2.43	0.48
2:F:221:GLN:HA	2:F:221:GLN:HE21	1.78	0.48
2:F:88:PRO:HD2	2:F:89:GLU:OE2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:SER:O	1:B:215:GLN:HG3	2.13	0.48
2:F:360:PRO:HD3	2:F:368:TYR:CE2	2.48	0.48
1:B:383:MET:O	1:B:384:LYS:C	2.52	0.48
2:D:14:VAL:HG11	2:D:24:GLN:HB2	1.95	0.48
2:E:360:PRO:HD3	2:E:368:TYR:CD1	2.49	0.48
2:E:404:VAL:O	2:E:408:ARG:HG3	2.14	0.48
1:A:453:LEU:HD13	1:A:461:ILE:HG23	1.96	0.48
1:B:225:ALA:HA	1:B:228:TYR:CE2	2.49	0.48
2:D:360:PRO:HD3	2:D:368:TYR:CE2	2.48	0.48
2:F:319:ASP:O	2:F:322:PRO:HD2	2.14	0.48
1:A:100:GLY:HA2	1:A:256:TYR:CD1	2.49	0.47
1:A:166:LEU:HD13	1:A:342:VAL:HG12	1.95	0.47
1:C:30:ARG:HA	1:C:86:ASP:O	2.13	0.47
1:C:481:SER:O	1:C:485:THR:HB	2.14	0.47
2:D:32:ILE:O	2:D:33:LEU:HB2	2.14	0.47
2:E:116:ILE:HA	2:E:238:THR:OG1	2.15	0.47
2:E:409:LYS:HZ2	2:E:450:ASP:HA	1.78	0.47
2:F:96:ASN:HD22	2:F:100:GLU:CB	2.27	0.47
1:C:187:LYS:HE3	1:C:224:ASP:HB3	1.96	0.47
1:C:34:ILE:HD11	1:C:79:ASP:CB	2.41	0.47
1:A:245:LEU:O	1:A:246:ALA:C	2.51	0.47
1:B:311:LYS:HD2	1:B:312:MET:O	2.13	0.47
1:B:443:ALA:O	1:B:446:TYR:HB3	2.14	0.47
1:B:45:ARG:HD3	1:B:45:ARG:HH11	1.53	0.47
1:C:313:ASN:OD1	1:C:315:ALA:HB3	2.14	0.47
2:F:36:LEU:HD23	2:F:36:LEU:N	2.30	0.47
2:F:80:ALA:HB1	2:F:81:PRO:HD2	1.94	0.47
2:F:82:ILE:HD13	2:F:98:ILE:HG22	1.96	0.47
1:B:240:ALA:N	1:B:241:PRO:CD	2.77	0.47
1:B:481:SER:O	1:B:485:THR:HB	2.14	0.47
2:D:129:GLU:OE1	2:D:129:GLU:HA	2.14	0.47
2:D:63:MET:HE3	2:D:228:ALA:HA	1.96	0.47
2:F:93:ARG:NH2	2:F:106:GLY:O	2.48	0.47
2:F:357:ILE:HD12	2:F:362:ILE:HG21	1.95	0.47
1:A:444:VAL:CG1	1:A:469:LEU:HD13	2.44	0.47
2:E:438:ILE:O	2:E:442:GLN:HB2	2.15	0.47
3:G:210:ALA:O	3:G:213:ILE:N	2.47	0.47
1:A:188:ARG:HE	1:A:437:ALA:HB2	1.80	0.47
1:A:40:ARG:CG	1:A:40:ARG:HH11	2.27	0.47
1:C:211:SER:HB3	2:F:126:MET:CE	2.45	0.47
2:E:33:LEU:HD13	2:E:117:HIS:CG	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:374:VAL:O	2:E:377:ILE:HG22	2.14	0.47
2:F:346:PRO:HG3	2:F:418:PHE:HZ	1.80	0.47
1:C:289:PRO:HG2	3:G:268:GLY:HA2	1.95	0.47
1:C:441:GLN:O	1:C:445:ILE:HG12	2.14	0.47
2:D:432:VAL:HG13	2:D:433:PRO:HD2	1.97	0.47
2:E:259:PHE:CE2	2:E:263:GLN:HG2	2.50	0.47
1:A:107:VAL:HB	1:A:116:ASP:HB3	1.97	0.47
1:C:59:LEU:HD23	1:C:82:ILE:CD1	2.44	0.47
1:A:376:SER:O	1:A:378:ALA:N	2.48	0.47
1:B:496:LYS:O	1:B:500:ILE:HG13	2.15	0.47
1:B:34:ILE:HG23	2:E:32:ILE:CD1	2.44	0.47
1:A:307:GLU:OE1	2:E:190:THR:HB	2.15	0.47
1:C:445:ILE:HG22	1:C:449:VAL:CG2	2.44	0.47
2:D:368:TYR:CE1	2:D:372:ARG:HG3	2.50	0.47
2:E:253:LEU:O	2:E:306:SER:HA	2.14	0.47
1:B:33:SER:HB2	2:E:52:HIS:O	2.14	0.47
2:F:467:VAL:O	2:F:470:ALA:HB3	2.14	0.47
1:C:288:PRO:HG3	3:G:272:LEU:HD23	1.96	0.47
1:A:209:LYS:HE3	1:A:211:SER:CB	2.45	0.47
2:E:393:MET:O	2:E:393:MET:HE2	2.15	0.47
2:F:205:VAL:HG23	2:F:215:VAL:HG21	1.96	0.47
1:B:171:ARG:HH11	1:B:171:ARG:HG3	1.79	0.46
1:B:210:ARG:O	1:B:211:SER:C	2.53	0.46
2:E:204:GLY:O	2:E:205:VAL:C	2.54	0.46
2:E:204:GLY:C	2:E:206:ILE:N	2.68	0.46
2:F:455:GLN:H	2:F:455:GLN:CD	2.18	0.46
2:F:462:PRO:HG2	2:F:465:GLU:HG3	1.96	0.46
1:A:49:ALA:O	1:A:50:GLU:HB2	2.13	0.46
1:B:469:LEU:HG	1:B:473:ILE:HD11	1.98	0.46
1:B:27:GLU:OE1	1:B:90:ARG:HD3	2.16	0.46
1:C:102:GLU:HG2	1:C:122:GLY:C	2.36	0.46
1:C:292:GLU:O	1:C:293:ALA:CB	2.63	0.46
1:C:156:LEU:HD11	1:C:428:LEU:CD1	2.45	0.46
1:C:91:THR:HG22	1:C:93:ALA:HB3	1.97	0.46
2:E:409:LYS:NZ	2:E:450:ASP:HA	2.30	0.46
1:A:313:ASN:OD1	1:A:316:PHE:HD2	1.98	0.46
1:B:284:LEU:CD2	2:E:274:ARG:HD3	2.45	0.46
2:E:41:ARG:O	2:E:42:GLU:C	2.53	0.46
2:E:82:ILE:HB	2:E:116:ILE:CD1	2.45	0.46
1:A:485:THR:HG22	1:A:486:ASP:N	2.29	0.46
1:B:358:TYR:C	1:B:360:GLY:N	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:469:LYS:O	2:D:473:LEU:HG	2.15	0.46
1:B:283:LEU:CD1	2:E:277:SER:HA	2.46	0.46
3:G:209:LEU:O	3:G:210:ALA:C	2.52	0.46
3:G:259:THR:O	3:G:263:ILE:HG13	2.16	0.46
1:C:251:CYS:O	1:C:255:GLU:HG3	2.16	0.46
2:E:242:TYR:C	2:E:244:ARG:H	2.18	0.46
2:E:431:LEU:O	2:E:431:LEU:HD12	2.15	0.46
2:E:63:MET:CE	2:E:228:ALA:HA	2.46	0.46
1:A:142:VAL:HG22	1:A:161:ARG:O	2.16	0.46
1:A:51:GLU:OE2	1:A:90:ARG:HB3	2.16	0.46
1:B:179:ALA:O	1:B:182:THR:HB	2.14	0.46
1:B:34:ILE:HD12	1:B:35:GLY:H	1.81	0.46
1:B:381:ARG:HG2	1:B:488:LYS:HG3	1.97	0.46
1:C:180:ILE:HG22	1:C:184:ILE:HD12	1.96	0.46
2:D:237:LEU:HD21	2:D:295:ARG:HB2	1.97	0.46
2:E:112:GLN:NE2	2:E:242:TYR:HE2	2.13	0.46
2:E:146:TYR:O	2:E:357:ILE:HD11	2.16	0.46
2:F:237:LEU:HD13	2:F:296:ILE:HG12	1.98	0.46
1:A:36:ASP:O	1:A:284:LEU:HD13	2.16	0.46
1:A:78:ASN:OD1	1:A:80:LYS:HB3	2.15	0.46
1:B:209:LYS:NZ	2:E:356:ARG:HH12	2.05	0.46
2:E:61:ILE:O	2:E:61:ILE:HG13	2.14	0.46
2:F:151:LYS:HD3	2:F:328:HIS:O	2.15	0.46
1:B:286:ARG:HG2	2:E:275:ILE:HD12	1.98	0.46
1:C:432:GLN:O	1:C:433:TYR:HB2	2.16	0.46
1:C:67:GLU:HB3	1:C:68:PRO:HD2	1.98	0.46
2:D:289:MET:SD	2:D:324:THR:HG22	2.56	0.46
2:D:440:GLY:O	2:D:444:ILE:HG13	2.16	0.46
2:F:310:ILE:HD13	2:F:325:THR:HG21	1.98	0.46
1:C:30:ARG:HE	1:C:87:ILE:CD1	2.18	0.46
1:C:476:HIS:N	1:C:476:HIS:ND1	2.64	0.46
2:D:154:LEU:HD13	2:D:165:LEU:HD23	1.96	0.46
2:F:339:ILE:CG2	2:F:344:ILE:HB	2.46	0.46
2:F:469:LYS:O	2:F:473:LEU:HG	2.16	0.46
1:A:213:VAL:O	1:A:216:LEU:HB3	2.16	0.45
1:A:240:ALA:HB3	1:A:241:PRO:HD3	1.97	0.45
2:D:130:GLN:HE22	2:D:356:ARG:HD3	1.81	0.45
2:E:343:GLY:O	2:E:345:TYR:HD1	1.99	0.45
2:F:221:GLN:HA	2:F:221:GLN:NE2	2.31	0.45
2:F:345:TYR:HA	2:F:346:PRO:C	2.36	0.45
1:C:474:SER:OG	1:C:475:GLN:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:231:ARG:O	2:D:234:LEU:N	2.50	0.45
2:D:35:ALA:HB1	2:D:46:VAL:CG1	2.47	0.45
2:E:120:ALA:HB1	2:E:121:PRO:HD2	1.98	0.45
1:A:339:PRO:O	1:A:343:ILE:HG13	2.16	0.45
1:C:83:LYS:HB3	2:F:52:HIS:CE1	2.52	0.45
2:E:388:ILE:HG23	2:E:393:MET:CG	2.43	0.45
2:E:405:SER:OG	2:E:406:ARG:N	2.49	0.45
1:C:289:PRO:CD	3:G:268:GLY:HA2	2.46	0.45
2:F:275:ILE:HD11	3:G:271:ALA:HB1	1.93	0.45
1:A:245:LEU:C	1:A:247:PRO:HD2	2.36	0.45
1:B:389:THR:HA	1:B:392:LEU:HG	1.97	0.45
2:E:443:GLN:HA	2:E:446:ALA:HB3	1.99	0.45
2:E:316:ASP:OD2	3:G:255:GLN:NE2	2.49	0.45
2:F:29:LEU:HD11	2:F:58:VAL:HG13	1.98	0.45
1:A:412:ALA:HA	1:A:415:GLN:HB3	1.98	0.45
1:A:413:ALA:O	1:A:416:GLN:HB3	2.17	0.45
1:A:62:MET:HE2	1:A:76:PHE:HZ	1.81	0.45
1:B:465:GLU:O	1:B:469:LEU:HB2	2.17	0.45
2:D:345:TYR:HA	2:D:346:PRO:C	2.37	0.45
2:F:200:MET:CG	2:F:206:ILE:HG12	2.46	0.45
1:A:59:LEU:HD11	1:A:81:LEU:HD12	1.99	0.45
1:B:141:SER:HB2	1:B:143:ARG:NH1	2.31	0.45
1:C:338:ILE:O	1:C:339:PRO:C	2.51	0.45
2:D:452:LEU:HD12	2:D:457:PHE:CZ	2.52	0.45
2:E:281:TYR:CZ	2:E:321:ALA:HB2	2.52	0.45
2:E:402:LEU:O	2:E:406:ARG:HG3	2.16	0.45
2:F:409:LYS:HD3	2:F:457:PHE:HE2	1.77	0.45
1:A:385:GLN:OE1	1:A:488:LYS:HB2	2.17	0.45
1:A:85:GLY:O	1:A:86:ASP:C	2.53	0.45
1:B:400:VAL:HB	1:B:418:LEU:CD2	2.45	0.45
2:D:201:ILE:HD13	2:D:208:LEU:HD11	1.98	0.45
2:F:243:PHE:O	2:F:249:GLN:HB2	2.16	0.45
2:E:390:ILE:HG13	3:G:25:MET:CG	2.47	0.45
1:A:179:ALA:O	1:A:182:THR:HB	2.17	0.45
1:B:76:PHE:HB3	1:B:242:LEU:HD21	1.99	0.45
1:B:271:LEU:HD12	1:B:325:PRO:HB2	1.98	0.45
1:C:488:LYS:HG2	1:C:489:ILE:N	2.28	0.45
2:E:321:ALA:N	2:E:322:PRO:HD2	2.32	0.45
3:G:82:HIS:CD2	3:G:82:HIS:N	2.85	0.45
1:B:212:THR:O	1:B:216:LEU:HB2	2.17	0.45
1:B:353:GLU:HG3	1:B:366:ASN:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:SER:CB	2:D:126:MET:CE	2.95	0.45
2:D:170:ILE:O	2:D:174:ALA:HB3	2.17	0.45
2:D:63:MET:HE1	2:D:227:GLY:O	2.17	0.45
2:E:85:PRO:HD2	2:E:95:MET:CE	2.47	0.45
3:G:234:ASN:HA	3:G:237:LYS:HB2	1.98	0.45
1:A:133:ALA:HB1	1:A:134:PRO:HD2	1.99	0.44
1:A:166:LEU:HD13	1:A:342:VAL:CG1	2.47	0.44
1:A:97:VAL:HG11	1:A:249:SER:HB2	1.99	0.44
1:C:219:ARG:HD3	1:C:433:TYR:HE1	1.81	0.44
1:B:300:TYR:HA	1:B:303:SER:OG	2.17	0.44
1:C:404:ALA:HB1	1:C:410:LEU:HD11	1.99	0.44
2:D:470:ALA:O	2:D:474:ALA:N	2.51	0.44
2:E:35:ALA:HB2	2:E:82:ILE:HG13	1.99	0.44
2:F:359:ASP:OD1	2:F:360:PRO:HD2	2.17	0.44
2:E:276:PRO:HD2	3:G:266:ILE:HD11	1.98	0.44
1:C:311:LYS:HE3	1:C:318:GLY:O	2.17	0.44
1:C:158:PRO:HB3	1:C:379:GLN:HG3	1.99	0.44
1:C:26:GLU:HB3	1:C:46:ASN:ND2	2.32	0.44
1:B:84:GLU:CD	2:E:54:GLY:HA2	2.38	0.44
2:F:50:ALA:O	2:F:51:GLN:HB3	2.17	0.44
2:F:96:ASN:HB2	2:F:100:GLU:N	2.32	0.44
1:A:140:ILE:CG2	1:A:313:ASN:HA	2.47	0.44
1:A:460:LYS:HD2	1:A:460:LYS:N	2.32	0.44
1:B:140:ILE:HG13	1:B:143:ARG:NH1	2.32	0.44
1:B:286:ARG:HA	2:E:275:ILE:HD12	1.99	0.44
1:B:420:ARG:O	1:B:423:ARG:N	2.50	0.44
2:D:108:ILE:HG22	2:D:110:THR:HG23	2.00	0.44
2:D:386:ASP:HB3	3:G:12:SER:CB	2.48	0.44
1:A:244:TYR:HE1	1:A:301:LEU:HD11	1.83	0.44
1:A:45:ARG:HA	1:A:45:ARG:HD3	1.67	0.44
1:B:423:ARG:HE	1:B:458:PRO:CG	2.31	0.44
1:C:245:LEU:O	1:C:246:ALA:C	2.56	0.44
2:D:95:MET:HG2	2:D:99:GLY:HA2	1.99	0.44
1:A:379:GLN:HB2	1:A:384:LYS:HE3	2.00	0.44
2:D:461:GLY:HA3	2:D:462:PRO:HD3	1.74	0.44
2:E:147:ALA:HB2	2:E:357:ILE:HD13	1.98	0.44
1:B:218:LYS:NZ	2:E:129:GLU:OE2	2.51	0.44
1:B:437:ALA:O	1:B:438:ILE:C	2.54	0.44
2:D:319:ASP:O	2:D:320:PRO:C	2.55	0.44
2:D:400:ASP:O	2:D:404:VAL:HG23	2.18	0.44
2:D:433:PRO:HG2	2:D:436:GLU:CG	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:LEU:O	1:A:396:GLN:HG3	2.18	0.44
1:C:185:ASN:HB2	1:C:435:PRO:HB3	2.00	0.44
2:D:298:THR:HG23	2:D:303:SER:HA	1.98	0.44
2:D:366:GLU:O	2:D:370:VAL:HG23	2.17	0.44
2:E:433:PRO:HG2	2:E:436:GLU:CG	2.48	0.44
3:G:13:ILE:HD13	3:G:242:MET:SD	2.57	0.44
1:C:390:MET:HE2	1:C:428:LEU:HD11	1.99	0.44
1:C:51:GLU:HG2	1:C:52:MET:N	2.33	0.44
1:C:68:PRO:HD3	2:D:15:ALA:HB2	2.00	0.44
1:C:303:SER:HB2	2:D:222:MET:HB3	2.00	0.44
2:D:412:ARG:O	2:D:415:SER:OG	2.33	0.44
2:E:166:ILE:O	2:E:170:ILE:HG13	2.18	0.44
2:E:432:VAL:HA	2:E:433:PRO:HD3	1.81	0.44
2:F:407:ALA:O	2:F:411:GLN:HB2	2.18	0.44
1:A:463:LYS:HD3	1:A:508:PHE:CZ	2.52	0.43
1:A:62:MET:HE2	1:A:76:PHE:CZ	2.53	0.43
1:C:489:ILE:HG22	1:C:494:ASP:HB2	1.99	0.43
2:D:462:PRO:HD2	2:D:465:GLU:HG3	2.00	0.43
2:D:96:ASN:HB2	2:D:100:GLU:N	2.27	0.43
2:F:348:VAL:O	2:F:350:PRO:HD3	2.17	0.43
1:A:151:LYS:HE2	1:A:427:LEU:O	2.17	0.43
1:B:389:THR:HA	1:B:392:LEU:CG	2.49	0.43
1:B:400:VAL:HG12	1:B:418:LEU:HD11	2.00	0.43
1:C:193:THR:O	1:C:195:GLU:OE1	2.36	0.43
2:D:103:ASP:O	2:D:104:GLU:HB2	2.18	0.43
2:F:105:ARG:CZ	2:F:208:LEU:HD23	2.47	0.43
1:A:68:PRO:HD3	2:E:15:ALA:HB2	1.99	0.43
1:B:400:VAL:CG1	1:B:418:LEU:HD11	2.47	0.43
1:A:307:GLU:HG3	2:E:223:ASN:CG	2.39	0.43
2:E:136:GLY:HA2	2:E:432:VAL:O	2.18	0.43
2:F:257:ASN:OD1	2:F:259:PHE:HB3	2.17	0.43
3:G:23:MET:HB2	3:G:232:MET:HE2	1.99	0.43
1:A:283:LEU:HD11	1:A:293:ALA:HB1	1.99	0.43
1:A:420:ARG:HA	1:A:420:ARG:HD3	1.78	0.43
1:B:389:THR:HG22	1:B:392:LEU:HD12	2.00	0.43
1:C:209:LYS:HE3	1:C:211:SER:OG	2.18	0.43
2:D:189:ARG:O	2:D:192:GLU:HB2	2.18	0.43
2:D:412:ARG:HG3	2:D:412:ARG:NH1	2.33	0.43
2:E:114:ALA:HB3	2:E:238:THR:CG2	2.47	0.43
1:B:286:ARG:HG2	2:E:275:ILE:CD1	2.49	0.43
2:E:397:SER:C	2:E:399:GLU:H	2.20	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:TYR:CD1	1:A:421:GLY:HA3	2.54	0.43
1:A:471:HIS:ND1	1:A:475:GLN:HG3	2.32	0.43
1:C:32:LEU:HD21	1:C:42:HIS:HB2	2.00	0.43
2:E:376:LYS:O	2:E:379:GLN:HB2	2.18	0.43
1:B:136:ILE:HG13	2:F:190:THR:HG23	1.99	0.43
2:F:188:GLU:H	2:F:221:GLN:NE2	2.15	0.43
2:F:31:PRO:O	2:F:34:ASN:HB2	2.19	0.43
2:F:47:LEU:HD23	2:F:62:ALA:HA	2.01	0.43
1:C:107:VAL:O	1:C:115:ILE:HG12	2.18	0.43
2:E:161:GLY:O	2:E:162:LYS:C	2.57	0.43
2:E:310:ILE:HD11	2:E:329:LEU:HD11	2.00	0.43
2:F:270:ALA:O	2:F:273:GLY:N	2.44	0.43
2:F:346:PRO:HG3	2:F:418:PHE:CZ	2.52	0.43
1:A:210:ARG:HD2	1:A:210:ARG:HH11	1.69	0.43
1:B:32:LEU:HD21	1:B:42:HIS:HB2	2.00	0.43
2:F:439:LYS:HG2	2:F:443:GLN:NE2	2.33	0.43
1:A:180:ILE:O	1:A:181:ASP:C	2.57	0.43
1:A:52:MET:CG	1:A:95:VAL:HG22	2.49	0.43
1:C:147:GLN:OE1	1:C:438:ILE:HD13	2.19	0.43
1:C:169:GLY:O	1:C:175:LYS:HE2	2.18	0.43
2:D:410:ILE:HG23	2:D:441:PHE:CE1	2.54	0.43
2:E:359:ASP:O	2:E:362:ILE:N	2.45	0.43
2:F:141:ASP:HB3	2:F:434:LEU:HD13	2.01	0.43
2:F:144:ALA:N	2:F:145:PRO:CD	2.82	0.43
1:B:213:VAL:O	1:B:217:VAL:HG13	2.18	0.43
1:C:423:ARG:CD	1:C:461:ILE:HD11	2.49	0.43
2:E:136:GLY:HA3	2:E:431:LEU:CD1	2.48	0.43
1:A:251:CYS:O	1:A:255:GLU:HG3	2.18	0.43
1:A:99:VAL:HG23	1:A:253:MET:HA	2.01	0.43
1:B:255:GLU:HG2	1:B:258:ARG:CZ	2.49	0.43
1:B:151:LYS:NZ	1:B:427:LEU:O	2.47	0.43
1:B:430:GLN:HB3	1:B:430:GLN:HE21	1.50	0.43
1:C:269:ASP:HA	1:C:270:ASP:HA	1.79	0.43
1:C:49:ALA:N	1:C:66:LEU:HD11	2.34	0.43
1:C:78:ASN:HD21	1:C:80:LYS:HD3	1.84	0.43
1:C:164:ARG:HH22	2:D:189:ARG:HD3	1.83	0.43
2:D:93:ARG:NH1	2:D:108:ILE:HG12	2.33	0.43
2:E:105:ARG:NE	2:E:208:LEU:HD23	2.33	0.43
2:F:400:ASP:O	2:F:404:VAL:HG23	2.19	0.43
2:F:89:GLU:HG2	2:F:110:THR:CG2	2.44	0.43
1:A:288:PRO:HA	1:A:289:PRO:HD3	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:VAL:HG12	1:B:115:ILE:HD11	2.00	0.42
2:D:445:LEU:HD23	2:D:445:LEU:HA	1.91	0.42
2:F:95:MET:HG3	2:F:99:GLY:HA2	2.00	0.42
1:C:208:GLN:HB2	1:C:208:GLN:HE21	1.38	0.42
1:C:353:GLU:O	1:C:364:ALA:HB1	2.19	0.42
2:D:209:LYS:HA	2:D:209:LYS:HD3	1.83	0.42
2:D:266:SER:CB	2:D:282:GLN:NE2	2.82	0.42
2:D:425:THR:HB	2:D:459:MET:HE2	2.00	0.42
2:D:94:ILE:HG22	2:D:102:ILE:HD11	2.01	0.42
2:E:425:THR:C	2:E:427:HIS:N	2.72	0.42
2:E:67:GLU:H	2:E:67:GLU:HG3	1.16	0.42
2:F:122:GLU:OE1	2:F:122:GLU:HA	2.19	0.42
1:A:115:ILE:O	2:D:124:VAL:HG13	2.18	0.42
1:A:96:ASP:HA	1:A:128:ARG:HA	2.01	0.42
1:A:383:MET:O	1:A:386:VAL:HG23	2.19	0.42
1:A:485:THR:C	1:A:487:GLY:H	2.23	0.42
1:A:78:ASN:ND2	1:A:80:LYS:HD2	2.34	0.42
1:B:294:TYR:CE2	1:B:338:ILE:HD13	2.53	0.42
1:B:165:GLU:O	1:B:325:PRO:HD2	2.19	0.42
2:D:38:VAL:HG11	2:D:69:LEU:CD2	2.49	0.42
3:G:209:LEU:O	3:G:212:ILE:N	2.51	0.42
1:A:340:THR:O	1:A:344:SER:HB3	2.19	0.42
2:E:12:ARG:NH2	2:E:24:GLN:OE1	2.50	0.42
2:E:296:ILE:HD13	2:E:306:SER:HB2	2.02	0.42
2:F:196:LEU:O	2:F:200:MET:HB2	2.19	0.42
2:F:387:ILE:HG13	2:F:387:ILE:H	1.62	0.42
1:A:184:ILE:HD12	1:A:223:ALA:CB	2.50	0.42
1:B:385:GLN:NE2	1:B:489:ILE:HB	2.34	0.42
2:E:29:LEU:HA	2:E:30:PRO:HD2	1.92	0.42
2:E:461:GLY:HA3	2:E:462:PRO:HD3	1.73	0.42
2:F:136:GLY:HA3	2:F:431:LEU:HD11	1.99	0.42
1:B:433:TYR:C	1:B:435:PRO:HD3	2.40	0.42
2:D:279:VAL:HG12	2:D:279:VAL:O	2.20	0.42
2:E:189:ARG:HB2	2:E:192:GLU:HG3	2.02	0.42
2:F:452:LEU:HD22	2:F:470:ALA:CB	2.49	0.42
1:A:137:ILE:HD11	2:E:103:ASP:HA	2.02	0.42
1:A:74:VAL:HG13	1:A:241:PRO:HG3	2.00	0.42
1:B:434:SER:N	1:B:435:PRO:CD	2.81	0.42
2:E:189:ARG:O	2:E:190:THR:C	2.58	0.42
1:A:247:PRO:HG2	1:A:274:GLN:NE2	2.35	0.42
1:A:56:SER:O	1:A:58:GLY:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:ARG:HE	1:A:90:ARG:HB3	1.73	0.42
2:D:112:GLN:NE2	2:D:242:TYR:HE1	2.18	0.42
2:E:95:MET:HA	2:E:100:GLU:O	2.20	0.42
2:D:387:ILE:HG21	3:G:19:ILE:CD1	2.50	0.42
1:A:267:ILE:HA	1:A:324:LEU:O	2.20	0.42
1:A:32:LEU:HD21	1:A:42:HIS:HB2	2.02	0.42
1:B:381:ARG:HA	1:B:384:LYS:HB2	2.01	0.42
1:B:485:THR:O	1:B:486:ASP:C	2.58	0.42
1:C:224:ASP:OD1	1:C:227:LYS:HE3	2.19	0.42
2:D:63:MET:CE	2:D:228:ALA:HA	2.50	0.42
2:E:387:ILE:HG22	2:E:388:ILE:HD13	2.02	0.42
3:G:254:ARG:O	3:G:258:ILE:HG13	2.20	0.42
1:A:139:ARG:C	1:A:140:ILE:HG22	2.40	0.42
1:A:383:MET:HG3	1:A:387:ALA:HB2	2.02	0.42
1:C:49:ALA:O	1:C:50:GLU:HB2	2.19	0.42
2:D:200:MET:CE	2:D:215:VAL:HG21	2.50	0.42
2:D:35:ALA:HB1	2:D:46:VAL:HG13	2.02	0.42
2:D:396:LEU:HD22	2:D:400:ASP:HB2	2.01	0.42
2:D:475:GLU:HA	2:D:475:GLU:OE1	2.20	0.42
2:F:385:GLN:HA	2:F:388:ILE:HG12	2.01	0.42
2:D:386:ASP:HB3	3:G:12:SER:HB2	2.02	0.42
1:A:338:ILE:N	1:A:339:PRO:CD	2.83	0.41
2:D:397:SER:O	2:D:398:GLU:C	2.58	0.41
2:E:122:GLU:HB2	2:E:125:GLU:HG3	2.01	0.41
2:E:396:LEU:CB	2:E:401:LYS:HG2	2.50	0.41
1:A:206:ILE:O	1:A:273:LYS:HD2	2.20	0.41
2:D:145:PRO:HB2	2:D:357:ILE:HD11	2.01	0.41
2:D:412:ARG:C	2:D:414:LEU:N	2.73	0.41
2:E:182:VAL:HG21	2:E:240:ALA:HB2	2.01	0.41
2:E:412:ARG:NH1	2:E:454:GLU:OE1	2.53	0.41
1:A:105:GLY:HA2	1:A:226:MET:O	2.21	0.41
1:A:103:LEU:O	1:A:106:ARG:HB2	2.20	0.41
1:A:485:THR:C	1:A:487:GLY:N	2.73	0.41
1:B:206:ILE:HA	1:B:234:ALA:O	2.21	0.41
1:B:75:VAL:HG21	1:B:82:ILE:HD12	2.02	0.41
1:B:78:ASN:ND2	1:B:80:LYS:HE2	2.35	0.41
1:C:374:VAL:CG1	1:C:378:ALA:HB2	2.51	0.41
2:E:360:PRO:HD3	2:E:368:TYR:CG	2.56	0.41
2:E:388:ILE:HD12	2:E:396:LEU:HD11	2.01	0.41
2:E:441:PHE:O	2:E:445:LEU:HG	2.19	0.41
1:A:292:GLU:HB2	1:A:294:TYR:HD2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:336:ALA:HB3	1:B:339:PRO:HD2	2.02	0.41
1:C:151:LYS:HE2	1:C:436:MET:SD	2.60	0.41
1:C:151:LYS:HG3	1:C:430:GLN:OE1	2.21	0.41
1:C:442:VAL:HG11	1:C:489:ILE:HD11	2.01	0.41
1:C:467:ALA:O	1:C:470:SER:HB2	2.20	0.41
2:D:86:VAL:HG11	2:D:114:ALA:HB3	2.02	0.41
2:D:349:ASP:HA	2:D:350:PRO:HD2	1.85	0.41
2:D:13:ILE:HD12	2:D:73:GLN:HB3	2.03	0.41
2:D:38:VAL:HG22	2:D:75:VAL:HG22	2.02	0.41
1:A:353:GLU:CD	1:A:366:ASN:HD22	2.23	0.41
1:B:423:ARG:HH21	1:B:458:PRO:HD3	1.86	0.41
2:D:201:ILE:CD1	2:D:208:LEU:HD11	2.50	0.41
2:D:360:PRO:HD3	2:D:368:TYR:CD2	2.56	0.41
2:E:158:ALA:C	2:E:160:VAL:N	2.72	0.41
2:E:63:MET:HE3	2:E:228:ALA:HA	2.02	0.41
2:E:340:ALA:O	2:E:343:GLY:N	2.42	0.41
2:E:346:PRO:HG3	2:E:418:PHE:HZ	1.83	0.41
2:E:387:ILE:HG22	2:E:388:ILE:N	2.36	0.41
2:F:357:ILE:O	2:F:359:ASP:N	2.48	0.41
2:F:38:VAL:HG11	2:F:69:LEU:CD2	2.50	0.41
1:A:344:SER:O	2:E:222:MET:CE	2.69	0.41
1:A:498:LYS:O	1:A:502:THR:HG23	2.21	0.41
1:B:423:ARG:O	1:B:426:GLU:N	2.51	0.41
1:C:104:LEU:HD21	1:C:257:PHE:CZ	2.56	0.41
1:C:164:ARG:HD2	1:C:164:ARG:HH11	1.41	0.41
1:C:139:ARG:HB3	1:C:311:LYS:O	2.19	0.41
1:C:465:GLU:O	1:C:469:LEU:HB2	2.21	0.41
1:C:484:ARG:HH11	1:C:484:ARG:HD3	1.76	0.41
2:D:390:ILE:HD13	3:G:16:ILE:CD1	2.50	0.41
2:E:282:GLN:NE2	2:E:282:GLN:H	2.19	0.41
2:F:423:VAL:HG12	2:F:423:VAL:O	2.20	0.41
3:G:217:LEU:O	3:G:221:THR:HG23	2.20	0.41
1:B:30:ARG:HA	1:B:86:ASP:O	2.21	0.41
2:D:112:GLN:NE2	2:D:242:TYR:CE1	2.88	0.41
2:D:52:HIS:CD2	2:D:58:VAL:HG12	2.56	0.41
2:F:251:VAL:HG12	2:F:252:LEU:N	2.35	0.41
2:F:434:LEU:O	2:F:438:ILE:HG12	2.21	0.41
1:A:74:VAL:CG1	1:A:241:PRO:HG3	2.51	0.41
1:C:19:ALA:O	1:C:21:THR:HG23	2.21	0.41
1:C:45:ARG:HH11	1:C:45:ARG:HD2	1.67	0.41
2:D:203:SER:OG	2:D:205:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:398:GLU:HA	2:D:401:LYS:CG	2.51	0.41
2:D:401:LYS:HG2	2:D:401:LYS:H	1.72	0.41
2:E:165:LEU:HD22	2:E:335:LEU:HD21	2.02	0.41
2:E:397:SER:O	2:E:399:GLU:N	2.54	0.41
3:G:241:GLU:O	3:G:245:LYS:HB2	2.21	0.41
1:A:129:VAL:HG12	1:A:249:SER:HA	2.03	0.41
1:A:294:TYR:CE2	1:A:338:ILE:HD13	2.56	0.41
1:A:398:ARG:HH11	1:A:398:ARG:HD2	1.53	0.41
1:B:201:CYS:O	1:B:229:THR:HA	2.21	0.41
2:E:422:GLU:C	2:E:424:PHE:N	2.74	0.41
2:E:97:VAL:HG13	2:E:232:VAL:HG12	2.02	0.41
2:F:81:PRO:O	2:F:82:ILE:C	2.58	0.41
1:A:403:PHE:O	1:A:404:ALA:C	2.59	0.41
1:A:440:GLU:HG2	1:A:473:ILE:HD11	2.03	0.41
1:B:361:ILE:HD13	1:B:429:LYS:HE2	2.02	0.41
1:C:468:PHE:CZ	1:C:501:VAL:HG12	2.56	0.41
2:D:417:PRO:HA	2:D:459:MET:HE1	2.02	0.41
2:D:84:ILE:HD12	2:D:95:MET:CE	2.50	0.41
2:E:139:VAL:HG21	2:E:348:VAL:HB	2.02	0.41
2:F:442:GLN:O	2:F:445:LEU:HB2	2.20	0.41
3:G:10:LEU:O	3:G:14:LYS:HG3	2.20	0.41
3:G:2:THR:O	3:G:3:LEU:C	2.57	0.41
1:A:485:THR:O	1:A:487:GLY:N	2.54	0.41
1:A:67:GLU:HB3	1:A:68:PRO:HD2	2.03	0.41
2:D:190:THR:O	2:D:191:ARG:C	2.60	0.41
2:F:228:ALA:O	2:F:232:VAL:HG22	2.21	0.41
3:G:42:ARG:HG2	3:G:219:GLU:OE2	2.20	0.41
1:A:294:TYR:HB2	1:A:337:TYR:CE2	2.54	0.40
1:A:268:TYR:HB2	1:A:325:PRO:HA	2.02	0.40
1:B:187:LYS:HE3	1:B:227:LYS:NZ	2.37	0.40
1:B:452:TYR:CD2	1:B:501:VAL:HG21	2.56	0.40
1:A:215:GLN:HE21	2:D:128:VAL:HA	1.86	0.40
2:D:27:GLU:H	2:D:27:GLU:HG3	1.77	0.40
2:D:65:GLY:HA3	2:D:67:GLU:OE2	2.22	0.40
2:E:210:ASP:OD1	2:E:211:ALA:N	2.55	0.40
2:E:231:ARG:O	2:E:234:LEU:N	2.50	0.40
2:E:329:LEU:O	2:E:356:ARG:CZ	2.69	0.40
1:A:441:GLN:O	1:A:445:ILE:HG12	2.21	0.40
1:B:99:VAL:HG13	1:B:256:TYR:HB2	2.02	0.40
1:C:340:THR:O	1:C:341:ASN:C	2.59	0.40
1:C:342:VAL:HA	1:C:345:ILE:HD12	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:368:TYR:O	2:D:372:ARG:HG2	2.22	0.40
2:E:82:ILE:CG2	2:E:116:ILE:HD13	2.51	0.40
2:F:167:MET:HB2	2:F:420:VAL:HG11	2.02	0.40
2:F:471:ASP:O	2:F:474:ALA:N	2.53	0.40
3:G:13:ILE:HD13	3:G:242:MET:HG2	2.02	0.40
1:A:147:GLN:OE1	1:A:438:ILE:HD13	2.21	0.40
1:B:107:VAL:O	1:B:115:ILE:HG12	2.20	0.40
1:B:304:ARG:HD3	1:B:304:ARG:HH11	1.64	0.40
2:D:274:ARG:HH11	2:D:274:ARG:HD2	1.50	0.40
2:E:185:GLY:HA3	2:E:188:GLU:HG3	2.02	0.40
2:E:434:LEU:CD1	2:E:438:ILE:HD11	2.52	0.40
1:A:479:LEU:O	1:A:482:LYS:HB2	2.22	0.40
1:B:239:ALA:HB1	1:B:241:PRO:HD2	2.03	0.40
1:B:366:ASN:ND2	1:B:369:LEU:HG	2.36	0.40
1:B:376:SER:O	1:B:384:LYS:HE2	2.22	0.40
1:B:439:GLU:HA	1:B:442:VAL:CG2	2.52	0.40
2:D:200:MET:HE3	2:D:215:VAL:HG21	2.03	0.40
2:D:97:VAL:HG11	2:D:231:ARG:HB2	2.04	0.40
2:D:281:TYR:CD2	2:D:320:PRO:HG2	2.56	0.40
2:D:281:TYR:HB3	2:D:285:LEU:HD12	2.03	0.40
2:D:402:LEU:O	2:D:406:ARG:HG3	2.21	0.40
2:E:227:GLY:O	2:E:231:ARG:HG2	2.21	0.40
2:E:55:GLU:O	2:E:56:SER:HB2	2.21	0.40
1:A:180:ILE:HD11	1:A:216:LEU:CD2	2.52	0.40
1:A:408:SER:O	1:A:409:ASP:HB2	2.20	0.40
1:B:221:THR:HG22	1:B:222:ASP:N	2.36	0.40
1:B:283:LEU:CD1	2:E:277:SER:CA	2.98	0.40
2:D:105:ARG:NH1	2:D:208:LEU:HD23	2.36	0.40
2:D:63:MET:CE	2:D:97:VAL:HG11	2.51	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	485/553 (88%)	443 (91%)	35 (7%)	7 (1%)	11	46
1	B	475/553 (86%)	427 (90%)	41 (9%)	7 (2%)	10	45
1	C	490/553 (89%)	444 (91%)	38 (8%)	8 (2%)	9	44
2	D	465/528 (88%)	418 (90%)	44 (10%)	3 (1%)	25	66
2	E	464/528 (88%)	407 (88%)	48 (10%)	9 (2%)	8	38
2	F	464/528 (88%)	432 (93%)	30 (6%)	2 (0%)	34	72
3	G	116/298 (39%)	97 (84%)	18 (16%)	1 (1%)	17	56
All	All	2959/3541 (84%)	2668 (90%)	254 (9%)	37 (1%)	12	48

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	407	GLY
2	E	393	MET
1	A	57	SER
1	A	405	GLN
1	A	409	ASP
1	B	364	ALA
1	C	332	GLY
1	C	408	SER
1	C	411	ASP
1	C	476	HIS
2	D	28	GLY
2	E	161	GLY
2	E	205	VAL
3	G	81	ILE
1	A	364	ALA
1	A	404	ALA
1	B	236	ALA
1	B	452	TYR
2	E	121	PRO
2	E	455	GLN
1	B	411	ASP
1	C	405	GLN
1	C	475	GLN
2	D	474	ALA
2	E	122	GLU
2	F	327	ALA
1	A	484	ARG
1	B	359	LYS
1	C	409	ASP

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Mol	Chain	Res	Type
2	E	33	LEU
1	B	458	PRO
2	E	28	GLY
2	E	279	VAL
1	B	68	PRO
2	F	279	VAL
2	D	279	VAL
1	A	246	ALA

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	393/444 (88%)	351 (89%)	42 (11%)	6	24
1	B	388/444 (87%)	341 (88%)	47 (12%)	5	20
1	C	397/444 (89%)	369 (93%)	28 (7%)	14	39
2	D	377/417 (90%)	346 (92%)	31 (8%)	11	34
2	E	376/417 (90%)	343 (91%)	33 (9%)	10	31
2	F	376/417 (90%)	354 (94%)	22 (6%)	19	45
3	G	102/251 (41%)	92 (90%)	10 (10%)	8	27
All	All	2409/2834 (85%)	2196 (91%)	213 (9%)	10	31

All (213) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	THR
1	A	40	ARG
1	A	45	ARG
1	A	47	VAL
1	A	48	GLN
1	A	50	GLU
1	A	56	SER
1	A	80	LYS
1	A	94	ILE

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Mol	Chain	Res	Type
1	A	99	VAL
1	A	101	GLU
1	A	102	GLU
1	A	121	ILE
1	A	140	ILE
1	A	143	ARG
1	A	151	LYS
1	A	164	ARG
1	A	173	THR
1	A	188	ARG
1	A	193	THR
1	A	195	GLU
1	A	211	SER
1	A	219	ARG
1	A	256	TYR
1	A	270	ASP
1	A	344	SER
1	A	367	VAL
1	A	371	VAL
1	A	380	THR
1	A	386	VAL
1	A	393	GLU
1	A	409	ASP
1	A	417	LEU
1	A	420	ARG
1	A	436	MET
1	A	444	VAL
1	A	457	GLU
1	A	472	VAL
1	A	474	SER
1	A	479	LEU
1	A	497	LEU
1	A	499	GLU
1	B	38	ILE
1	B	47	VAL
1	B	52	MET
1	B	79	ASP
1	B	80	LYS
1	B	123	SER
1	B	141	SER
1	B	143	ARG
1	B	145	PRO

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Mol	Chain	Res	Type
1	B	164	ARG
1	B	173	THR
1	B	186	GLN
1	B	188	ARG
1	B	189	PHE
1	B	193	THR
1	B	211	SER
1	B	216	LEU
1	B	217	VAL
1	B	218	LYS
1	B	221	THR
1	B	227	LYS
1	B	233	SER
1	B	256	TYR
1	B	270	ASP
1	B	298	VAL
1	B	299	PHE
1	B	335	SER
1	B	349	GLN
1	B	351	PHE
1	B	371	VAL
1	B	374	VAL
1	B	376	SER
1	B	380	THR
1	B	381	ARG
1	B	399	GLU
1	B	416	GLN
1	B	423	ARG
1	B	430	GLN
1	B	442	VAL
1	B	444	VAL
1	B	454	ASP
1	B	474	SER
1	B	479	LEU
1	B	482	LYS
1	B	484	ARG
1	B	490	SER
1	B	505	LEU
1	C	45	ARG
1	C	47	VAL
1	C	56	SER
1	C	63	SER

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Mol	Chain	Res	Type
1	C	64	LEU
1	C	87	ILE
1	C	101	GLU
1	C	164	ARG
1	C	189	PHE
1	C	195	GLU
1	C	208	GLN
1	C	227	LYS
1	C	270	ASP
1	C	282	SER
1	C	298	VAL
1	C	334	VAL
1	C	349	GLN
1	C	399	GLU
1	C	400	VAL
1	C	406	PHE
1	C	440	GLU
1	C	444	VAL
1	C	474	SER
1	C	477	GLN
1	C	479	LEU
1	C	501	VAL
1	C	502	THR
1	C	505	LEU
2	D	27	GLU
2	D	37	GLU
2	D	56	SER
2	D	67	GLU
2	D	95	MET
2	D	97	VAL
2	D	112	GLN
2	D	137	ILE
2	D	139	VAL
2	D	166	ILE
2	D	199	GLU
2	D	205	VAL
2	D	223	ASN
2	D	232	VAL
2	D	249	GLN
2	D	266	SER
2	D	282	GLN
2	D	306	SER

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Mol	Chain	Res	Type
2	D	322	PRO
2	D	336	SER
2	D	361	ASN
2	D	365	SER
2	D	388	ILE
2	D	397	SER
2	D	400	ASP
2	D	401	LYS
2	D	405	SER
2	D	423	VAL
2	D	431	LEU
2	D	452	LEU
2	D	475	GLU
2	E	9	THR
2	E	67	GLU
2	E	95	MET
2	E	127	SER
2	E	128	VAL
2	E	132	ILE
2	E	133	LEU
2	E	139	VAL
2	E	148	LYS
2	E	155	PHE
2	E	164	VAL
2	E	194	ASN
2	E	213	SER
2	E	215	VAL
2	E	223	ASN
2	E	225	PRO
2	E	257	ASN
2	E	282	GLN
2	E	293	GLN
2	E	297	THR
2	E	306	SER
2	E	358	MET
2	E	365	SER
2	E	385	GLN
2	E	387	ILE
2	E	391	LEU
2	E	393	MET
2	E	394	ASP
2	E	395	GLU

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Mol	Chain	Res	Type
2	E	412	ARG
2	E	431	LEU
2	E	438	ILE
2	E	452	LEU
2	F	10	THR
2	F	27	GLU
2	F	42	GLU
2	F	67	GLU
2	F	95	MET
2	F	112	GLN
2	F	127	SER
2	F	139	VAL
2	F	166	ILE
2	F	191	ARG
2	F	200	MET
2	F	210	ASP
2	F	223	ASN
2	F	232	VAL
2	F	261	PHE
2	F	292	MET
2	F	386	ASP
2	F	387	ILE
2	F	397	SER
2	F	405	SER
2	F	428	LEU
2	F	455	GLN
3	G	4	LYS
3	G	11	LYS
3	G	22	SER
3	G	44	TYR
3	G	77	LEU
3	G	82	HIS
3	G	209	LEU
3	G	214	TYR
3	G	221	THR
3	G	254	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	215	GLN
1	A	349	GLN

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Mol	Chain	Res	Type
1	A	396	GLN
1	A	432	GLN
1	B	48	GLN
1	B	65	ASN
1	B	215	GLN
1	B	349	GLN
1	B	432	GLN
1	C	208	GLN
1	C	260	ASN
1	C	349	GLN
1	C	432	GLN
2	D	194	ASN
2	D	221	GLN
2	D	223	ASN
2	D	282	GLN
2	D	442	GLN
2	E	39	GLN
2	E	130	GLN
2	E	194	ASN
2	E	223	ASN
2	E	246	GLN
2	E	367	HIS
2	F	39	GLN
2	F	96	ASN
2	F	221	GLN
2	F	223	ASN
2	F	282	GLN
2	F	443	GLN
3	G	82	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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 ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	487/553 (88%)	0.77	46 (9%) 8 11	20, 20, 20, 20	0
1	B	479/553 (86%)	0.49	28 (5%) 23 23	20, 20, 20, 20	0
1	C	492/553 (88%)	0.49	22 (4%) 33 31	20, 20, 20, 20	0
2	D	467/528 (88%)	0.74	42 (8%) 9 11	20, 20, 20, 20	0
2	E	466/528 (88%)	0.88	63 (13%) 3 6	20, 20, 20, 20	0
2	F	466/528 (88%)	0.47	20 (4%) 35 32	20, 20, 20, 20	0
3	G	122/298 (40%)	0.74	13 (10%) 6 9	20, 20, 20, 20	0
All	All	2979/3541 (84%)	0.64	234 (7%) 12 14	20, 20, 20, 20	0

All (234) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	180	TYR	5.5
2	E	63	MET	5.4
2	E	179	GLY	4.8
2	D	297	THR	4.8
2	D	160	VAL	4.6
2	D	158	ALA	4.3
2	E	62	ALA	4.2
2	D	461	GLY	4.2
1	A	310	ALA	4.0
2	E	147	ALA	3.9
2	F	297	THR	3.9
2	D	97	VAL	3.9
2	E	233	ALA	3.8
1	C	289	PRO	3.8
2	E	236	GLY	3.7
1	C	379	GLN	3.7
2	D	393	MET	3.7

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Mol	Chain	Res	Type	RSRZ
2	E	240	ALA	3.6
2	E	146	TYR	3.6
2	E	92	GLY	3.6
1	B	34	ILE	3.6
2	E	51	GLN	3.5
1	B	163	GLN	3.5
2	E	64	ASP	3.5
1	A	489	ILE	3.5
1	C	489	ILE	3.4
2	E	461	GLY	3.4
2	F	462	PRO	3.4
1	A	162	GLY	3.4
2	E	249	GLN	3.4
1	A	352	LEU	3.4
1	A	328	GLU	3.4
1	A	311	LYS	3.3
2	D	256	ASP	3.3
1	B	82	ILE	3.2
3	G	23	MET	3.2
2	E	247	GLU	3.2
1	A	132	LYS	3.2
1	B	449	VAL	3.2
1	C	386	VAL	3.2
2	F	127	SER	3.2
1	B	105	GLY	3.2
2	D	296	ILE	3.2
2	D	220	GLY	3.2
2	D	328	HIS	3.2
2	D	232	VAL	3.1
1	B	436	MET	3.1
2	E	243	PHE	3.1
1	A	201	CYS	3.1
2	E	215	VAL	3.1
1	A	200	TYR	3.1
1	A	253	MET	3.1
2	E	178	GLY	3.0
3	G	211	ASN	3.0
1	C	173	THR	3.0
2	D	358	MET	3.0
2	F	260	ARG	3.0
2	D	391	LEU	3.0
2	E	462	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
3	G	24	LYS	3.0
1	A	309	ALA	3.0
2	D	333	THR	2.9
3	G	37	GLU	2.9
1	B	160	GLY	2.9
2	F	117	HIS	2.9
1	A	444	VAL	2.9
2	D	432	VAL	2.9
1	B	264	ALA	2.9
2	D	159	GLY	2.9
1	B	104	LEU	2.8
2	F	160	VAL	2.8
2	F	461	GLY	2.8
1	C	142	VAL	2.8
2	F	457	PHE	2.8
1	A	161	ARG	2.8
2	E	139	VAL	2.8
2	E	276	PRO	2.8
1	B	510	ALA	2.8
1	C	243	GLN	2.8
1	A	134	PRO	2.8
3	G	77	LEU	2.8
3	G	27	ALA	2.8
2	D	392	GLY	2.8
1	A	160	GLY	2.8
2	D	229	ARG	2.8
1	A	142	VAL	2.7
1	A	322	THR	2.7
1	B	164	ARG	2.7
3	G	232	MET	2.7
2	E	281	TYR	2.7
1	A	379	GLN	2.7
2	D	87	GLY	2.7
2	E	148	LYS	2.7
1	B	448	GLY	2.7
2	E	188	GLU	2.7
1	A	265	LEU	2.7
2	E	444	ILE	2.6
1	B	247	PRO	2.6
1	B	320	SER	2.6
2	D	254	PHE	2.6
2	E	328	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
2	F	298	THR	2.6
1	B	370	SER	2.6
1	A	199	LEU	2.6
1	B	103	LEU	2.6
1	C	99	VAL	2.6
2	E	420	VAL	2.6
1	A	406	PHE	2.6
1	C	161	ARG	2.6
2	E	52	HIS	2.6
3	G	1	ALA	2.6
1	A	409	ASP	2.6
1	B	509	GLU	2.6
1	A	34	ILE	2.5
2	F	302	GLY	2.5
2	F	311	TYR	2.5
2	F	156	GLY	2.5
1	C	376	SER	2.5
2	D	255	ILE	2.5
1	B	351	PHE	2.5
2	E	246	GLN	2.5
2	D	335	LEU	2.5
2	D	346	PRO	2.5
2	F	64	ASP	2.5
2	E	418	PHE	2.5
1	C	200	TYR	2.5
2	E	145	PRO	2.5
2	E	10	THR	2.5
2	E	94	ILE	2.5
1	A	208	GLN	2.5
1	C	234	ALA	2.5
2	E	213	SER	2.5
2	F	87	GLY	2.4
2	F	330	ASP	2.4
1	A	449	VAL	2.4
2	E	191	ARG	2.4
1	B	226	MET	2.4
1	A	504	PHE	2.4
2	E	130	GLN	2.4
1	A	163	GLN	2.4
1	A	365	ILE	2.4
2	E	159	GLY	2.4
2	E	283	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	173	THR	2.4
2	E	143	LEU	2.4
2	E	460	VAL	2.4
2	D	441	PHE	2.4
1	B	299	PHE	2.4
2	F	63	MET	2.4
1	A	133	ALA	2.4
1	A	321	LEU	2.3
1	C	19	ALA	2.3
1	B	161	ARG	2.3
3	G	218	LYS	2.3
1	C	128	ARG	2.3
2	E	219	TYR	2.3
2	F	116	ILE	2.3
2	D	117	HIS	2.3
3	G	214	TYR	2.3
1	C	383	MET	2.3
2	E	440	GLY	2.3
2	E	177	HIS	2.3
2	E	463	ILE	2.3
1	B	435	PRO	2.3
1	C	263	HIS	2.3
1	A	209	LYS	2.3
2	E	158	ALA	2.2
2	D	92	GLY	2.2
2	E	242	TYR	2.2
2	E	48	GLU	2.2
2	E	416	GLN	2.2
3	G	20	THR	2.2
1	A	202	ILE	2.2
2	E	417	PRO	2.2
1	B	489	ILE	2.2
1	A	89	LYS	2.2
2	D	452	LEU	2.2
2	E	192	GLU	2.2
2	E	419	GLN	2.2
1	A	320	SER	2.2
2	E	160	VAL	2.2
1	C	47	VAL	2.2
2	D	19	ALA	2.2
2	E	58	VAL	2.2
2	D	108	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	229	THR	2.1
1	A	408	SER	2.1
1	C	201	CYS	2.1
2	E	308	GLN	2.1
2	E	220	GLY	2.1
1	A	136	ILE	2.1
1	C	303	SER	2.1
1	A	327	ILE	2.1
2	D	81	PRO	2.1
2	D	146	TYR	2.1
2	E	443	GLN	2.1
1	A	262	LYS	2.1
2	F	441	PHE	2.1
1	A	206	ILE	2.1
3	G	220	SER	2.1
2	E	61	ILE	2.1
1	A	299	PHE	2.1
1	A	338	ILE	2.1
2	D	292	MET	2.1
2	E	232	VAL	2.1
2	D	130	GLN	2.1
2	D	190	THR	2.1
2	D	345	TYR	2.1
2	E	221	GLN	2.1
3	G	6	ILE	2.1
1	A	306	LEU	2.1
2	E	403	THR	2.1
2	D	330	ASP	2.1
1	B	101	GLU	2.1
1	B	230	ILE	2.1
2	D	331	ALA	2.1
1	A	53	VAL	2.1
1	B	142	VAL	2.0
2	E	230	ALA	2.0
1	C	253	MET	2.0
2	E	19	ALA	2.0
1	A	270	ASP	2.0
1	C	98	PRO	2.0
2	D	275	ILE	2.0
2	F	351	LEU	2.0
1	A	52	MET	2.0
2	E	66	THR	2.0

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Mol	Chain	Res	Type	RSRZ
2	F	346	PRO	2.0
2	D	307	VAL	2.0
1	B	162	GLY	2.0
2	D	459	MET	2.0
1	C	199	LEU	2.0
2	D	157	GLY	2.0
2	D	215	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.