



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:39 AM UTC

PDB ID : 3UQ7 / pdb_00003uq7
Title : X-ray structure of a pentameric ligand gated ion channel from *Erwinia chrysanthemi* (ELIC) mutant L240S F247L (L9S F16L) in presence of 10 mM cysteamine
Authors : Gonzalez-Gutierrez, G.; Lukk, T.; Agarwal, V.; Papke, D.; Nair, S.K.; Grosman, C.
Deposited on : 2011-11-19
Resolution : 3.80 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:

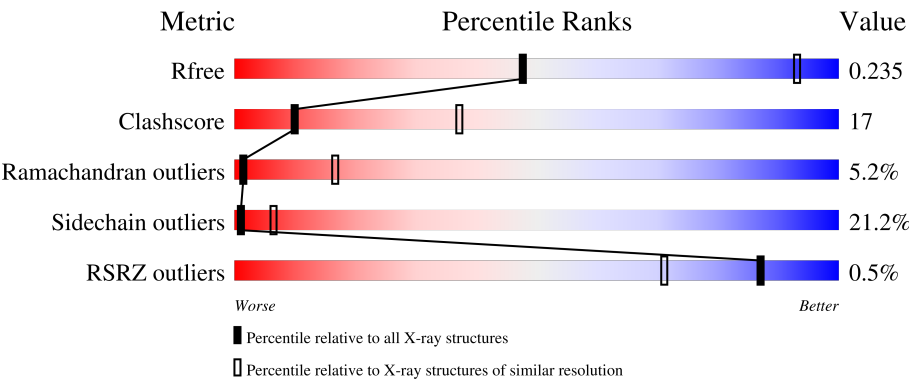
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 3.80 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}	180053	1065 (3.96-3.64)
Clashscore	190562	1012 (3.94-3.66)
Ramachandran outliers	187476	1048 (3.96-3.64)
Sidechain outliers	187428	1043 (3.96-3.64)
RSRZ outliers	180081	1064 (3.96-3.64)

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 $\leq 5\%$. 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	324	48%36%9%• 5%
1	B	324	% 48%32%13%• 5%
1	C	324	51%32%10%• 5%
1	D	324	48%33%12%• 5%
1	E	324	49%34%10%• 5%

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Mol	Chain	Length	Quality of chain
1	F	324	% 48% 34% 12% • 5%
1	G	324	% 48% 33% 13% • 5%
1	H	324	49% 32% 12% • 5%
1	I	324	% 47% 35% 11% • 5%
1	J	324	49% 33% 11% • 5%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 25000 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 Gamma-aminobutyric-acid receptor subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	B	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	C	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	D	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	E	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	F	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	G	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	H	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	I	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	J	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP E0SJQ4
A	0	SER	-	expression tag	UNP E0SJQ4
A	240	SER	LEU	engineered mutation	UNP E0SJQ4
A	247	LEU	PHE	engineered mutation	UNP E0SJQ4
B	-1	GLY	-	expression tag	UNP E0SJQ4
B	0	SER	-	expression tag	UNP E0SJQ4
B	240	SER	LEU	engineered mutation	UNP E0SJQ4
B	247	LEU	PHE	engineered mutation	UNP E0SJQ4
C	-1	GLY	-	expression tag	UNP E0SJQ4

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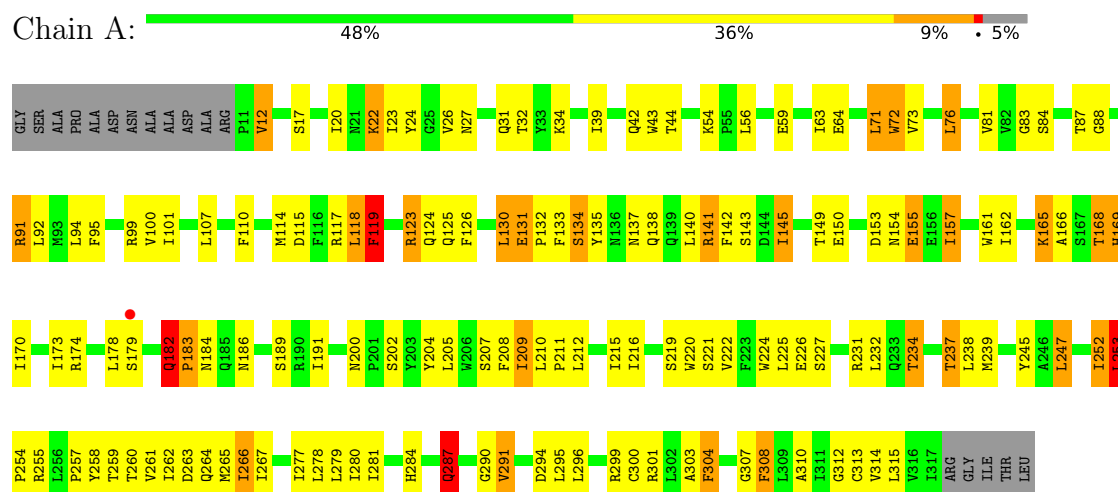
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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	SER	-	expression tag	UNP E0SJQ4
C	240	SER	LEU	engineered mutation	UNP E0SJQ4
C	247	LEU	PHE	engineered mutation	UNP E0SJQ4
D	-1	GLY	-	expression tag	UNP E0SJQ4
D	0	SER	-	expression tag	UNP E0SJQ4
D	240	SER	LEU	engineered mutation	UNP E0SJQ4
D	247	LEU	PHE	engineered mutation	UNP E0SJQ4
E	-1	GLY	-	expression tag	UNP E0SJQ4
E	0	SER	-	expression tag	UNP E0SJQ4
E	240	SER	LEU	engineered mutation	UNP E0SJQ4
E	247	LEU	PHE	engineered mutation	UNP E0SJQ4
F	-1	GLY	-	expression tag	UNP E0SJQ4
F	0	SER	-	expression tag	UNP E0SJQ4
F	240	SER	LEU	engineered mutation	UNP E0SJQ4
F	247	LEU	PHE	engineered mutation	UNP E0SJQ4
G	-1	GLY	-	expression tag	UNP E0SJQ4
G	0	SER	-	expression tag	UNP E0SJQ4
G	240	SER	LEU	engineered mutation	UNP E0SJQ4
G	247	LEU	PHE	engineered mutation	UNP E0SJQ4
H	-1	GLY	-	expression tag	UNP E0SJQ4
H	0	SER	-	expression tag	UNP E0SJQ4
H	240	SER	LEU	engineered mutation	UNP E0SJQ4
H	247	LEU	PHE	engineered mutation	UNP E0SJQ4
I	-1	GLY	-	expression tag	UNP E0SJQ4
I	0	SER	-	expression tag	UNP E0SJQ4
I	240	SER	LEU	engineered mutation	UNP E0SJQ4
I	247	LEU	PHE	engineered mutation	UNP E0SJQ4
J	-1	GLY	-	expression tag	UNP E0SJQ4
J	0	SER	-	expression tag	UNP E0SJQ4
J	240	SER	LEU	engineered mutation	UNP E0SJQ4
J	247	LEU	PHE	engineered mutation	UNP E0SJQ4

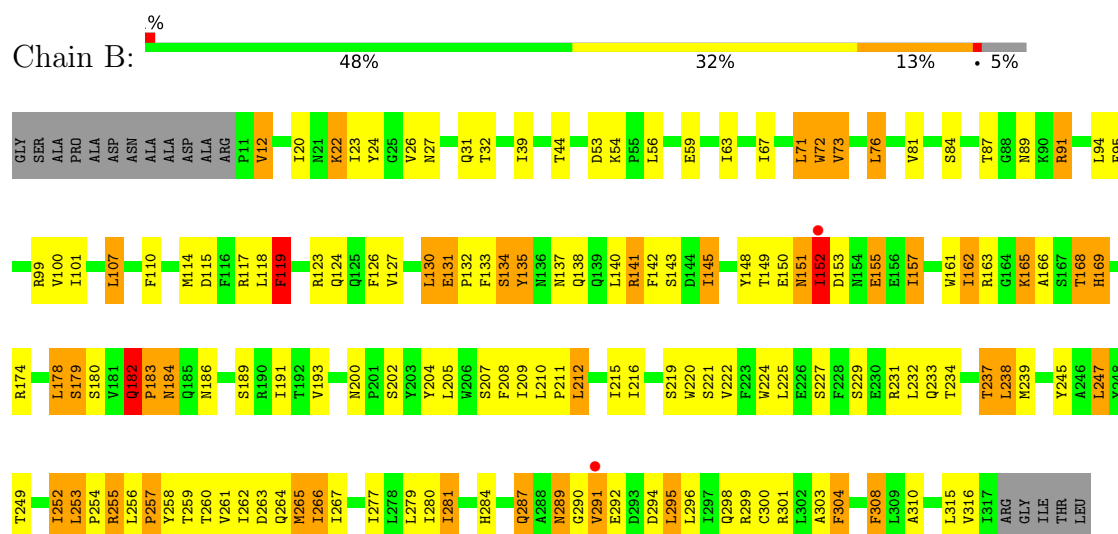
3 Residue-property plots

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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

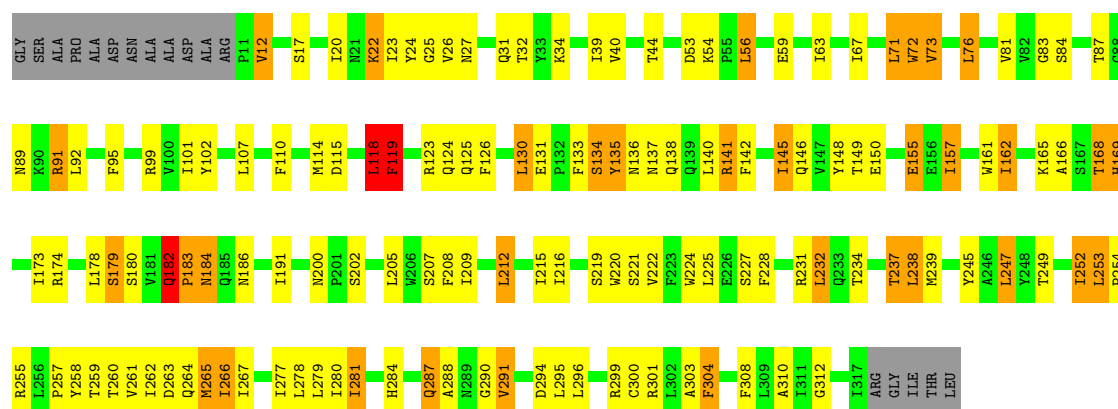


• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



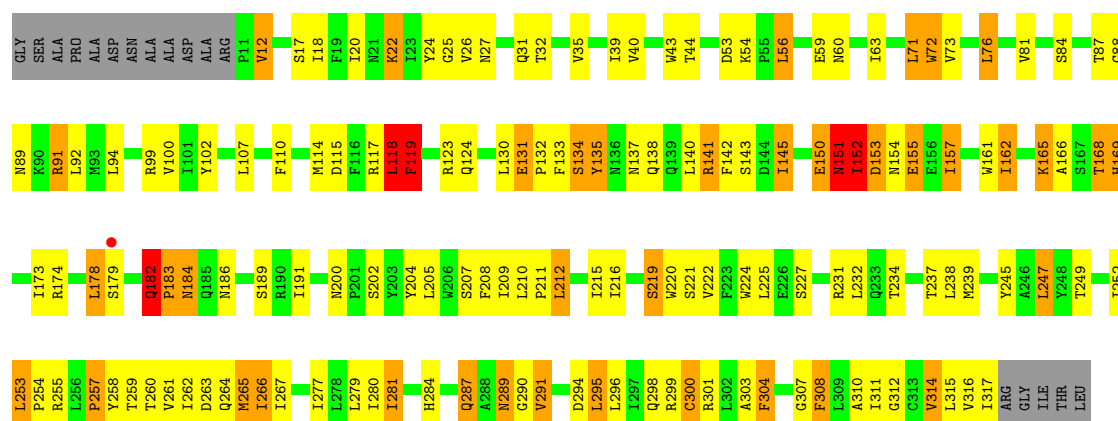
• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1





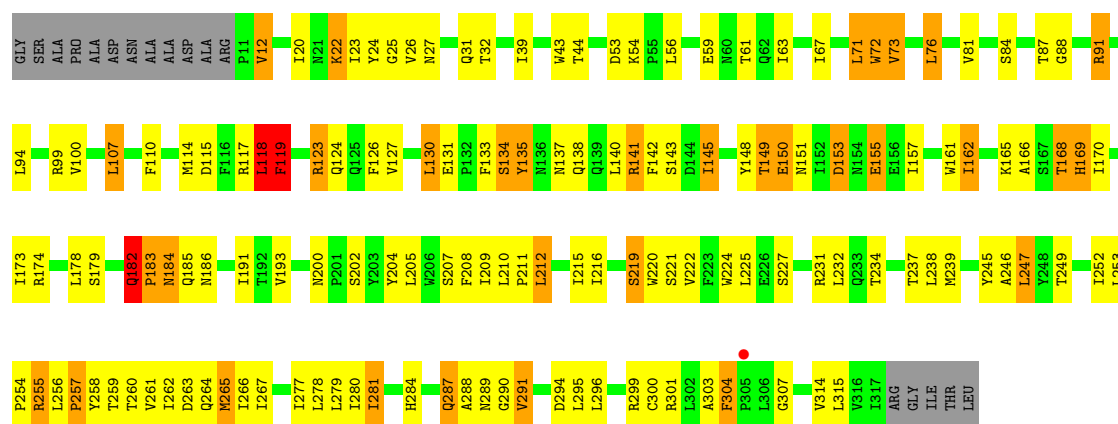
• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

Chain D: 48% 33% 12% • 5%



• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

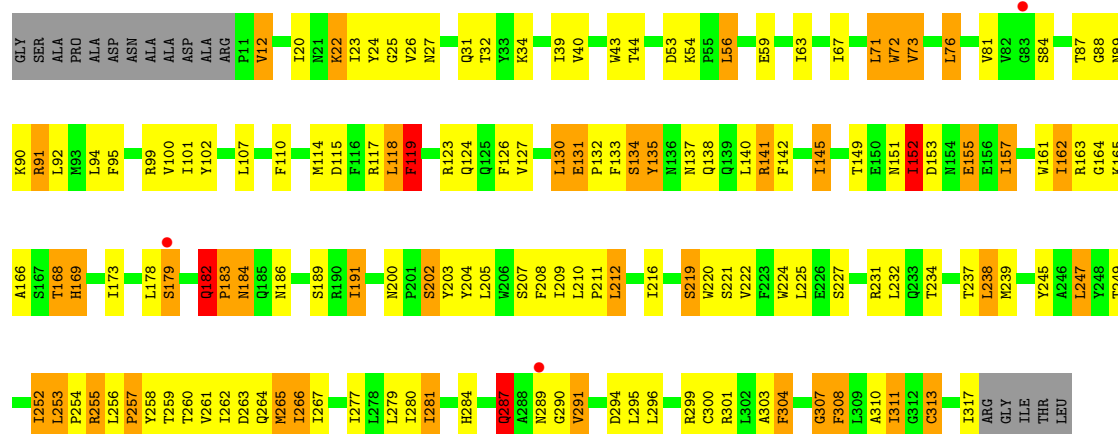
Chain E: 49% 34% 10% • 5%



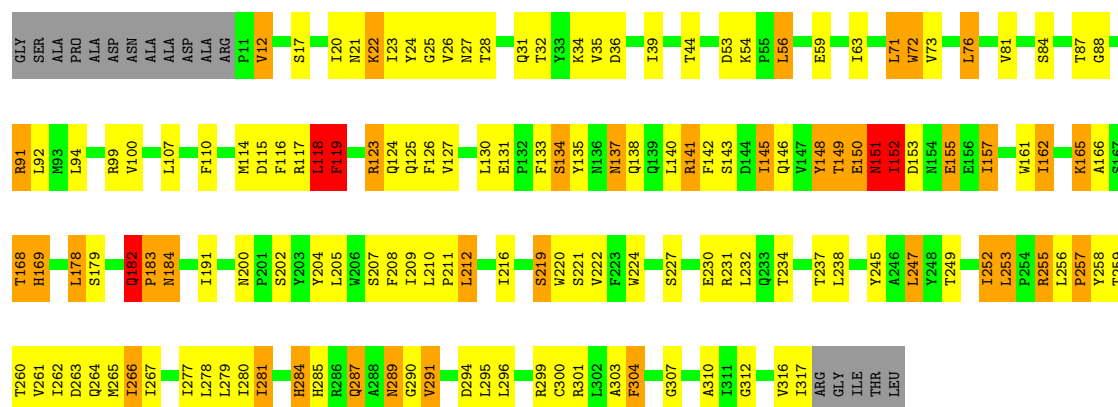
• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

Chain F: 48% 34% 12% • 5%

- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

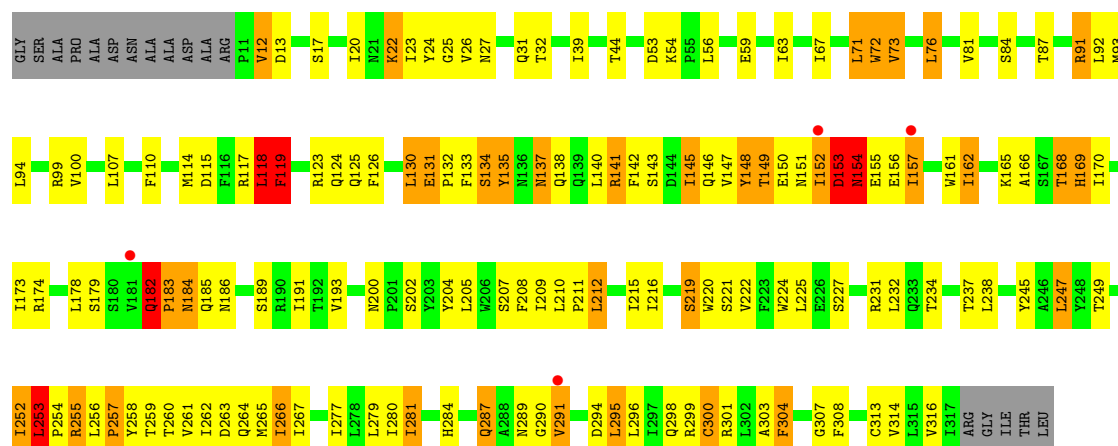


- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



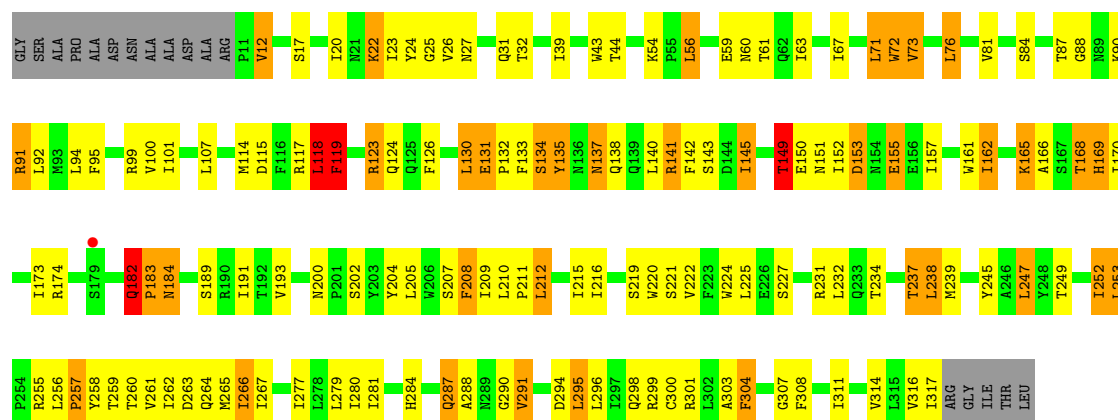
- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

Chain I: %



• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

Chain J: %



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.38Å 266.45Å 110.91Å 90.00° 109.47° 90.00°	Depositor
Resolution (Å)	19.97 – 3.80 19.97 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.97-3.80) 99.2 (19.97-3.80)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.29 (at 3.82Å)	Xtriage
Refinement program	PHENIX dev_897, REFMAC	Depositor
R, R_{free}	0.215 , 0.244 0.206 , 0.235	Depositor DCC
R_{free} test set	2810 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	110.2	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 68.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	25000	wwPDB-VP
Average B, all atoms (Å ²)	127.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% 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	0.70	0/2567	1.09	15/3499 (0.4%)
1	B	0.78	4/2567 (0.2%)	1.13	18/3499 (0.5%)
1	C	0.76	1/2567 (0.0%)	1.15	22/3499 (0.6%)
1	D	0.77	0/2567	1.13	20/3499 (0.6%)
1	E	0.74	1/2567 (0.0%)	1.14	16/3499 (0.5%)
1	F	0.70	0/2567	1.09	14/3499 (0.4%)
1	G	0.84	3/2567 (0.1%)	1.17	21/3499 (0.6%)
1	H	0.94	7/2567 (0.3%)	1.20	24/3499 (0.7%)
1	I	0.78	1/2567 (0.0%)	1.17	19/3499 (0.5%)
1	J	0.73	1/2567 (0.0%)	1.13	15/3499 (0.4%)
All	All	0.78	18/25670 (0.1%)	1.14	184/34990 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2
1	D	0	3
1	E	0	2
1	F	0	1
1	G	0	2
1	H	0	3
1	I	0	3
1	J	0	3
All	All	0	23

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	152	ILE	CA-C	14.06	1.70	1.52
1	G	289	ASN	CA-C	13.53	1.58	1.52
1	H	284	HIS	CE1-NE2	11.26	1.43	1.32
1	H	151	ASN	CA-C	11.21	1.67	1.52
1	H	152	ILE	N-CA	10.39	1.59	1.46
1	H	151	ASN	N-CA	8.44	1.57	1.46
1	G	152	ILE	CA-C	6.53	1.61	1.52
1	B	149	THR	CA-CB	6.37	1.63	1.53
1	B	127	VAL	CA-CB	-6.33	1.46	1.54
1	B	152	ILE	CA-C	6.03	1.59	1.52
1	H	150	GLU	CA-C	5.93	1.60	1.52
1	B	152	ILE	CA-CB	5.66	1.61	1.54
1	G	191	ILE	CA-CB	-5.35	1.48	1.54
1	H	148	TYR	C-O	-5.28	1.17	1.24
1	J	149	THR	CA-CB	5.26	1.62	1.53
1	C	149	THR	N-CA	5.23	1.52	1.46
1	E	149	THR	CA-CB	5.16	1.62	1.53
1	I	149	THR	CA-CB	5.04	1.61	1.53

All (184) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	154	ASN	N-CA-C	-15.16	78.50	110.80
1	H	148	TYR	CA-C-N	-11.81	103.69	122.23
1	H	148	TYR	C-N-CA	-11.81	103.69	122.23
1	I	153	ASP	CB-CA-C	11.36	133.02	110.42
1	J	314	VAL	N-CA-C	-10.23	103.99	113.71
1	G	153	ASP	CB-CA-C	-9.70	105.39	116.54
1	J	153	ASP	N-CA-C	8.68	120.85	108.00
1	D	153	ASP	CB-CA-C	-8.48	106.78	116.54
1	H	152	ILE	N-CA-C	8.27	126.55	109.34
1	C	150	GLU	N-CA-C	8.12	120.28	108.34
1	G	289	ASN	N-CA-C	7.99	120.77	108.30
1	F	131	GLU	CA-C-N	7.88	129.69	119.84
1	F	131	GLU	C-N-CA	7.88	129.69	119.84
1	E	150	GLU	N-CA-C	7.85	120.99	109.69
1	G	153	ASP	N-CA-C	7.70	120.02	108.31
1	D	84	SER	CA-C-N	7.51	129.01	120.98
1	D	84	SER	C-N-CA	7.51	129.01	120.98
1	H	148	TYR	O-C-N	-7.43	112.71	122.59
1	E	131	GLU	CA-C-N	7.38	129.07	119.84
1	E	131	GLU	C-N-CA	7.38	129.07	119.84
1	E	84	SER	CA-C-N	7.38	128.88	120.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	84	SER	C-N-CA	7.38	128.88	120.98
1	C	131	GLU	CA-C-N	7.32	128.99	119.84
1	C	131	GLU	C-N-CA	7.32	128.99	119.84
1	J	153	ASP	CB-CA-C	-7.28	106.15	116.34
1	I	84	SER	CA-C-N	7.27	128.76	120.98
1	I	84	SER	C-N-CA	7.27	128.76	120.98
1	E	12	VAL	N-CA-C	7.24	120.06	109.63
1	C	12	VAL	N-CA-C	7.23	120.04	109.63
1	G	131	GLU	CA-C-N	7.15	128.78	119.84
1	G	131	GLU	C-N-CA	7.15	128.78	119.84
1	H	84	SER	CA-C-N	7.15	128.63	120.98
1	H	84	SER	C-N-CA	7.15	128.63	120.98
1	C	148	TYR	N-CA-C	7.15	118.72	111.07
1	F	119	PHE	CA-C-N	-7.09	112.49	119.87
1	F	119	PHE	C-N-CA	-7.09	112.49	119.87
1	C	119	PHE	CA-C-N	-6.96	112.63	119.87
1	C	119	PHE	C-N-CA	-6.96	112.63	119.87
1	C	148	TYR	O-C-N	-6.94	114.92	122.07
1	G	84	SER	CA-C-N	6.91	128.38	120.98
1	G	84	SER	C-N-CA	6.91	128.38	120.98
1	J	131	GLU	CA-C-N	6.84	128.40	119.84
1	J	131	GLU	C-N-CA	6.84	128.40	119.84
1	C	148	TYR	CA-C-N	-6.84	110.57	121.86
1	C	148	TYR	C-N-CA	-6.84	110.57	121.86
1	I	119	PHE	CA-C-N	-6.74	112.86	119.87
1	I	119	PHE	C-N-CA	-6.74	112.86	119.87
1	J	12	VAL	N-CA-C	6.69	119.27	109.63
1	H	152	ILE	CA-C-N	-6.67	109.69	121.70
1	H	152	ILE	C-N-CA	-6.67	109.69	121.70
1	J	84	SER	CA-C-N	6.62	128.06	120.98
1	J	84	SER	C-N-CA	6.62	128.06	120.98
1	C	149	THR	N-CA-C	6.58	120.05	109.79
1	G	119	PHE	CA-C-N	-6.57	113.03	119.87
1	G	119	PHE	C-N-CA	-6.57	113.03	119.87
1	E	148	TYR	O-C-N	6.53	129.08	122.03
1	H	12	VAL	N-CA-C	6.52	119.02	109.63
1	H	119	PHE	CA-C-N	-6.52	113.09	119.87
1	H	119	PHE	C-N-CA	-6.52	113.09	119.87
1	H	131	GLU	CA-C-N	6.48	127.94	119.84
1	H	131	GLU	C-N-CA	6.48	127.94	119.84
1	A	84	SER	CA-C-N	6.45	127.89	120.98
1	A	84	SER	C-N-CA	6.45	127.89	120.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	131	GLU	CA-C-N	6.42	127.87	119.84
1	D	131	GLU	C-N-CA	6.42	127.87	119.84
1	D	12	VAL	N-CA-C	6.37	118.80	109.63
1	F	84	SER	CA-C-N	6.33	127.75	120.98
1	F	84	SER	C-N-CA	6.33	127.75	120.98
1	H	150	GLU	CA-C-N	6.26	133.50	121.54
1	H	150	GLU	C-N-CA	6.26	133.50	121.54
1	C	149	THR	N-CA-CB	6.25	119.45	110.45
1	B	89	ASN	N-CA-C	6.24	118.46	108.41
1	G	311	ILE	N-CA-C	-6.23	104.90	113.00
1	C	53	ASP	N-CA-C	-6.19	103.92	112.03
1	G	12	VAL	N-CA-C	6.18	118.52	109.63
1	H	151	ASN	N-CA-C	6.16	123.92	110.80
1	E	148	TYR	CA-C-N	6.15	130.47	121.31
1	E	148	TYR	C-N-CA	6.15	130.47	121.31
1	F	12	VAL	N-CA-C	6.14	118.47	109.63
1	J	119	PHE	CA-C-N	-6.11	113.52	119.87
1	J	119	PHE	C-N-CA	-6.11	113.52	119.87
1	G	152	ILE	N-CA-C	6.06	121.95	109.34
1	I	135	TYR	N-CA-C	6.06	118.72	107.99
1	A	119	PHE	CA-C-N	-6.06	113.57	119.87
1	A	119	PHE	C-N-CA	-6.06	113.57	119.87
1	I	314	VAL	N-CA-C	-6.06	106.59	112.29
1	I	125	GLN	N-CA-C	6.06	118.32	108.26
1	A	12	VAL	N-CA-C	6.06	118.35	109.63
1	D	152	ILE	N-CA-C	6.05	117.02	111.81
1	E	119	PHE	CA-C-N	-6.05	113.58	119.87
1	E	119	PHE	C-N-CA	-6.05	113.58	119.87
1	G	308	PHE	N-CA-C	-6.04	105.82	113.43
1	G	89	ASN	N-CA-C	6.03	118.12	108.41
1	B	315	LEU	N-CA-C	-5.99	106.13	113.50
1	A	287	GLN	N-CA-C	5.99	115.99	108.45
1	I	12	VAL	N-CA-C	5.97	118.23	109.63
1	B	148	TYR	O-C-N	5.96	128.47	122.03
1	C	308	PHE	N-CA-C	-5.96	105.92	113.43
1	E	135	TYR	N-CA-C	5.95	118.52	107.99
1	F	127	VAL	N-CA-C	5.94	117.31	108.46
1	D	119	PHE	CA-C-N	-5.91	113.56	120.12
1	D	119	PHE	C-N-CA	-5.91	113.56	120.12
1	G	135	TYR	N-CA-C	5.88	118.32	108.02
1	B	135	TYR	N-CA-C	5.87	118.30	108.02
1	B	131	GLU	CA-C-N	5.87	127.17	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	131	GLU	C-N-CA	5.87	127.17	119.84
1	A	131	GLU	CA-C-N	5.84	127.14	119.84
1	A	131	GLU	C-N-CA	5.84	127.14	119.84
1	F	150	GLU	N-CA-C	5.83	118.06	110.53
1	G	307	GLY	N-CA-C	-5.82	105.97	115.46
1	B	119	PHE	CA-C-N	-5.82	113.82	119.87
1	B	119	PHE	C-N-CA	-5.82	113.82	119.87
1	J	308	PHE	N-CA-C	-5.80	106.13	113.43
1	C	84	SER	CA-C-N	5.76	127.14	120.98
1	C	84	SER	C-N-CA	5.76	127.14	120.98
1	B	84	SER	CA-C-N	5.75	127.13	120.98
1	B	84	SER	C-N-CA	5.75	127.13	120.98
1	D	153	ASP	N-CA-C	5.74	117.04	108.31
1	I	300	CYS	N-CA-C	-5.72	106.53	112.93
1	H	151	ASN	CA-C-N	5.71	132.25	121.97
1	H	151	ASN	C-N-CA	5.71	132.25	121.97
1	F	125	GLN	N-CA-C	5.70	117.73	108.26
1	D	89	ASN	N-CA-C	5.69	117.56	108.41
1	C	135	TYR	N-CA-C	5.66	117.93	108.02
1	A	237	THR	N-CA-C	-5.64	105.66	112.54
1	J	237	THR	N-CA-C	-5.63	105.67	112.54
1	D	53	ASP	N-CA-C	-5.59	104.70	112.03
1	G	12	VAL	CB-CA-C	-5.55	102.27	111.32
1	I	131	GLU	CA-C-N	5.46	126.66	119.84
1	I	131	GLU	C-N-CA	5.46	126.66	119.84
1	F	308	PHE	N-CA-C	-5.45	106.56	113.43
1	C	237	THR	N-CA-C	-5.44	105.90	112.54
1	H	137	ASN	N-CA-C	5.43	116.82	109.11
1	B	12	VAL	N-CA-C	5.39	117.39	109.63
1	H	127	VAL	N-CA-C	5.38	116.41	108.45
1	C	125	GLN	N-CA-C	5.37	117.17	108.26
1	F	53	ASP	N-CA-C	-5.37	105.00	112.03
1	B	148	TYR	CA-C-N	5.35	129.76	121.26
1	B	148	TYR	C-N-CA	5.35	129.76	121.26
1	D	308	PHE	N-CA-C	-5.34	106.70	113.43
1	D	300	CYS	N-CA-C	-5.34	106.95	112.93
1	A	150	GLU	N-CA-C	5.33	118.40	110.14
1	J	135	TYR	N-CA-C	5.32	117.41	107.99
1	B	127	VAL	N-CA-C	5.32	115.78	108.12
1	I	253	LEU	CA-C-N	5.31	126.12	120.13
1	I	253	LEU	C-N-CA	5.31	126.12	120.13
1	I	137	ASN	N-CA-C	5.30	116.64	109.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	53	ASP	N-CA-C	-5.30	104.46	112.99
1	D	135	TYR	N-CA-C	5.29	117.28	108.02
1	A	307	GLY	N-CA-C	-5.28	106.85	115.46
1	G	53	ASP	N-CA-C	-5.28	104.64	111.71
1	C	150	GLU	CB-CA-C	-5.27	108.85	116.54
1	C	89	ASN	N-CA-C	5.26	117.33	108.96
1	D	150	GLU	N-CA-C	5.26	118.30	110.14
1	A	308	PHE	N-CA-C	-5.26	106.81	113.43
1	D	12	VAL	CB-CA-C	-5.25	102.77	111.32
1	E	127	VAL	N-CA-C	5.25	116.28	108.46
1	B	53	ASP	N-CA-C	-5.22	105.19	112.03
1	D	18	ILE	CB-CA-C	-5.21	104.21	110.99
1	D	307	GLY	N-CA-C	-5.21	106.96	115.46
1	C	136	ASN	N-CA-C	5.20	116.80	111.03
1	B	308	PHE	N-CA-C	-5.19	106.89	113.43
1	A	125	GLN	N-CA-C	5.19	116.88	108.26
1	H	12	VAL	CB-CA-C	-5.19	102.87	111.32
1	H	125	GLN	N-CA-C	5.18	116.85	108.26
1	F	307	GLY	N-CA-C	-5.15	107.07	115.46
1	J	307	GLY	N-CA-C	-5.10	107.15	115.46
1	G	127	VAL	N-CA-C	5.09	116.05	108.46
1	J	137	ASN	N-CA-C	5.07	116.31	109.11
1	D	315	LEU	N-CA-C	-5.07	105.94	111.82
1	I	307	GLY	N-CA-C	-5.07	107.19	115.46
1	I	308	PHE	N-CA-C	-5.07	107.04	113.43
1	E	53	ASP	N-CA-C	-5.07	104.92	111.71
1	G	287	GLN	N-CA-C	5.06	116.88	109.24
1	B	237	THR	N-CA-C	-5.06	106.37	112.54
1	E	12	VAL	CB-CA-C	-5.06	103.07	111.32
1	A	253	LEU	CA-C-N	5.05	125.84	120.13
1	A	253	LEU	C-N-CA	5.05	125.84	120.13
1	B	12	VAL	CB-CA-C	-5.04	103.10	111.32
1	F	135	TYR	N-CA-C	5.04	116.84	108.02
1	E	307	GLY	N-CA-C	-5.04	107.25	115.46
1	I	53	ASP	N-CA-C	-5.04	104.88	112.99
1	G	173	ILE	N-CA-C	5.03	115.22	108.17
1	H	307	GLY	N-CA-C	-5.01	107.30	115.46

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	LEU	Peptide
1	A	137	ASN	Peptide
1	B	137	ASN	Peptide
1	B	152	ILE	Peptide
1	C	118	LEU	Peptide
1	C	137	ASN	Peptide
1	D	118	LEU	Peptide
1	D	137	ASN	Peptide
1	D	152	ILE	Peptide
1	E	118	LEU	Peptide
1	E	137	ASN	Peptide
1	F	137	ASN	Peptide
1	G	137	ASN	Peptide
1	G	152	ILE	Peptide
1	H	118	LEU	Peptide
1	H	137	ASN	Peptide
1	H	149	THR	Peptide
1	I	118	LEU	Peptide
1	I	137	ASN	Peptide
1	I	148	TYR	Peptide
1	J	118	LEU	Peptide
1	J	137	ASN	Peptide
1	J	152	ILE	Peptide

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	2500	0	2474	91	0
1	B	2500	0	2474	110	0
1	C	2500	0	2474	91	0
1	D	2500	0	2474	97	0
1	E	2500	0	2474	89	0
1	F	2500	0	2474	91	0
1	G	2500	0	2474	99	0
1	H	2500	0	2474	98	0
1	I	2500	0	2474	118	0
1	J	2500	0	2474	81	0
All	All	25000	0	24740	867	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 17.

All (867) 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:289:ASN:ND2	1:B:292:GLU:OE2	1.86	1.07
1:I:154:ASN:HD22	1:I:155:GLU:N	1.52	1.06
1:I:154:ASN:HD22	1:I:155:GLU:H	1.08	1.00
1:H:151:ASN:N	1:H:153:ASP:OD2	1.94	0.99
1:H:152:ILE:N	1:H:153:ASP:OD1	1.99	0.95
1:B:169:HIS:ND1	1:I:168:THR:HB	1.82	0.94
1:I:154:ASN:ND2	1:I:155:GLU:H	1.68	0.92
1:I:151:ASN:H	1:I:153:ASP:HB2	1.36	0.89
1:B:140:LEU:HD13	1:B:191:ILE:HG13	1.56	0.87
1:H:140:LEU:HD13	1:H:191:ILE:HG13	1.57	0.86
1:B:224:TRP:HE1	1:B:301:ARG:HB3	1.39	0.86
1:F:140:LEU:HD13	1:F:191:ILE:HG13	1.58	0.85
1:J:224:TRP:HE1	1:J:301:ARG:HB3	1.39	0.85
1:B:91:ARG:HD2	1:C:134:SER:HB3	1.56	0.85
1:H:224:TRP:HE1	1:H:301:ARG:HB3	1.40	0.85
1:E:224:TRP:HE1	1:E:301:ARG:HB3	1.41	0.84
1:F:224:TRP:HE1	1:F:301:ARG:HB3	1.41	0.84
1:G:140:LEU:HD13	1:G:191:ILE:HG13	1.58	0.83
1:H:91:ARG:HD2	1:I:134:SER:HB3	1.61	0.82
1:H:150:GLU:C	1:H:153:ASP:OD2	2.22	0.82
1:D:205:LEU:HD23	1:D:209:ILE:HG13	1.61	0.82
1:C:91:ARG:HD2	1:D:134:SER:HB3	1.59	0.82
1:I:140:LEU:HD13	1:I:191:ILE:HG13	1.62	0.82
1:G:91:ARG:HD2	1:H:134:SER:HB3	1.62	0.81
1:D:224:TRP:HE1	1:D:301:ARG:HB3	1.44	0.81
1:C:140:LEU:HD13	1:C:191:ILE:HG13	1.63	0.80
1:A:134:SER:HB3	1:E:91:ARG:HD2	1.63	0.80
1:B:169:HIS:HD1	1:I:168:THR:HB	1.43	0.80
1:G:224:TRP:HE1	1:G:301:ARG:HB3	1.46	0.80
1:I:151:ASN:O	1:I:155:GLU:CD	2.24	0.80
1:I:224:TRP:HE1	1:I:301:ARG:HB3	1.46	0.80
1:C:224:TRP:HE1	1:C:301:ARG:HB3	1.45	0.79
1:D:91:ARG:HD2	1:E:134:SER:HB3	1.64	0.79
1:I:91:ARG:HD2	1:J:134:SER:HB3	1.63	0.79
1:F:205:LEU:HD23	1:F:209:ILE:HG13	1.64	0.78
1:C:205:LEU:HD23	1:C:209:ILE:HG13	1.64	0.78
1:F:91:ARG:HD2	1:G:134:SER:HB3	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:TRP:HE1	1:A:301:ARG:HB3	1.48	0.78
1:A:91:ARG:HD2	1:B:134:SER:HB3	1.66	0.78
1:I:154:ASN:ND2	1:I:155:GLU:N	2.30	0.77
1:I:155:GLU:HB3	1:I:161:TRP:CD1	2.20	0.77
1:D:284:HIS:HE1	1:D:291:VAL:HG12	1.50	0.77
1:I:147:VAL:O	1:I:149:THR:N	2.18	0.76
1:A:140:LEU:HD13	1:A:191:ILE:HG13	1.68	0.76
1:E:284:HIS:HE1	1:E:291:VAL:HG12	1.49	0.76
1:J:284:HIS:HE1	1:J:291:VAL:HG12	1.51	0.75
1:D:140:LEU:HD13	1:D:191:ILE:HG13	1.69	0.74
1:C:284:HIS:HE1	1:C:291:VAL:HG12	1.51	0.74
1:E:140:LEU:HD13	1:E:191:ILE:HG13	1.68	0.73
1:J:140:LEU:HD13	1:J:191:ILE:HG13	1.69	0.73
1:H:224:TRP:NE1	1:H:301:ARG:HB3	2.03	0.73
1:B:224:TRP:NE1	1:B:301:ARG:HB3	2.04	0.73
1:F:224:TRP:NE1	1:F:301:ARG:HB3	2.02	0.73
1:A:284:HIS:HE1	1:A:291:VAL:HG12	1.54	0.73
1:A:27:ASN:HB3	1:A:32:THR:HB	1.71	0.73
1:B:205:LEU:HD23	1:B:209:ILE:HG13	1.69	0.73
1:I:284:HIS:HE1	1:I:291:VAL:HG12	1.53	0.72
1:J:224:TRP:NE1	1:J:301:ARG:HB3	2.05	0.72
1:E:224:TRP:NE1	1:E:301:ARG:HB3	2.04	0.72
1:F:284:HIS:HE1	1:F:291:VAL:HG12	1.53	0.72
1:A:205:LEU:HD23	1:A:209:ILE:HG13	1.72	0.71
1:B:284:HIS:HE1	1:B:291:VAL:HG12	1.54	0.71
1:D:215:ILE:HG12	1:E:239:MET:HE3	1.72	0.71
1:H:205:LEU:HD23	1:H:209:ILE:HG13	1.71	0.71
1:E:205:LEU:HD23	1:E:209:ILE:HG13	1.72	0.70
1:F:134:SER:HB3	1:J:91:ARG:HD2	1.71	0.70
1:G:284:HIS:HE1	1:G:291:VAL:HG12	1.56	0.70
1:I:205:LEU:HD23	1:I:209:ILE:HG13	1.73	0.70
1:D:224:TRP:NE1	1:D:301:ARG:HB3	2.06	0.70
1:B:31:GLN:HG2	1:B:114:MET:HB2	1.74	0.69
1:G:224:TRP:NE1	1:G:301:ARG:HB3	2.07	0.69
1:C:224:TRP:NE1	1:C:301:ARG:HB3	2.06	0.69
1:A:224:TRP:NE1	1:A:301:ARG:HB3	2.08	0.69
1:D:27:ASN:HB3	1:D:32:THR:HB	1.74	0.69
1:D:165:LYS:HD3	1:D:166:ALA:H	1.58	0.69
1:G:205:LEU:HD23	1:G:209:ILE:HG13	1.75	0.69
1:B:119:PHE:HB2	1:B:260:THR:HB	1.76	0.68
1:J:205:LEU:HD23	1:J:209:ILE:HG13	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:27:ASN:HB3	1:F:32:THR:HB	1.76	0.68
1:J:119:PHE:HB2	1:J:260:THR:HB	1.75	0.68
1:E:44:THR:HA	1:E:99:ARG:HA	1.75	0.68
1:I:224:TRP:NE1	1:I:301:ARG:HB3	2.08	0.67
1:B:289:ASN:CG	1:B:292:GLU:HB3	2.19	0.67
1:A:44:THR:HA	1:A:99:ARG:HA	1.76	0.67
1:B:44:THR:HA	1:B:99:ARG:HA	1.77	0.67
1:B:165:LYS:HD3	1:B:166:ALA:H	1.57	0.67
1:H:44:THR:HA	1:H:99:ARG:HA	1.77	0.67
1:G:27:ASN:HB3	1:G:32:THR:HB	1.76	0.66
1:D:44:THR:HA	1:D:99:ARG:HA	1.78	0.66
1:D:284:HIS:CE1	1:D:291:VAL:HG12	2.31	0.66
1:I:165:LYS:HD3	1:I:166:ALA:H	1.60	0.66
1:C:44:THR:HA	1:C:99:ARG:HA	1.77	0.66
1:I:151:ASN:N	1:I:153:ASP:HB2	2.10	0.66
1:G:44:THR:HA	1:G:99:ARG:HA	1.78	0.65
1:C:27:ASN:HB3	1:C:32:THR:HB	1.77	0.65
1:I:27:ASN:HB3	1:I:32:THR:HB	1.77	0.65
1:A:165:LYS:HD3	1:A:166:ALA:H	1.61	0.65
1:B:27:ASN:HB3	1:B:32:THR:HB	1.78	0.65
1:G:114:MET:HG2	1:G:124:GLN:HE21	1.62	0.65
1:J:27:ASN:HB3	1:J:32:THR:HB	1.77	0.65
1:G:165:LYS:HD3	1:G:166:ALA:H	1.62	0.65
1:G:224:TRP:CE3	1:H:281:ILE:HG12	2.31	0.65
1:I:215:ILE:HG12	1:J:239:MET:HE3	1.77	0.65
1:E:165:LYS:HD3	1:E:166:ALA:H	1.61	0.65
1:G:224:TRP:HE3	1:H:281:ILE:HG12	1.62	0.65
1:J:165:LYS:HD3	1:J:166:ALA:H	1.62	0.65
1:F:44:THR:HA	1:F:99:ARG:HA	1.77	0.65
1:J:31:GLN:HG2	1:J:114:MET:HB2	1.79	0.65
1:I:44:THR:HA	1:I:99:ARG:HA	1.77	0.65
1:E:27:ASN:HB3	1:E:32:THR:HB	1.79	0.64
1:J:44:THR:HA	1:J:99:ARG:HA	1.79	0.64
1:H:27:ASN:HB3	1:H:32:THR:HB	1.79	0.64
1:E:31:GLN:HG2	1:E:114:MET:HB2	1.77	0.64
1:I:59:GLU:OE2	1:J:134:SER:OG	2.15	0.64
1:E:260:THR:O	1:E:264:GLN:HG3	1.98	0.64
1:H:249:THR:HG23	1:H:253:LEU:HD22	1.80	0.64
1:E:114:MET:HG2	1:E:124:GLN:HE21	1.62	0.64
1:D:114:MET:HG2	1:D:124:GLN:HE21	1.63	0.63
1:I:141:ARG:HG2	1:I:142:PHE:HD2	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:141:ARG:HG2	1:G:142:PHE:HD2	1.64	0.63
1:I:91:ARG:HB3	1:J:133:PHE:HE2	1.64	0.63
1:E:182:GLN:H	1:E:183:PRO:HD2	1.64	0.62
1:A:31:GLN:HG2	1:A:114:MET:HB2	1.80	0.62
1:H:165:LYS:HD3	1:H:166:ALA:H	1.63	0.62
1:I:31:GLN:HG2	1:I:114:MET:HB2	1.82	0.62
1:C:31:GLN:HG2	1:C:114:MET:HB2	1.81	0.62
1:J:182:GLN:H	1:J:183:PRO:HD2	1.63	0.62
1:F:155:GLU:HB2	1:F:161:TRP:CD1	2.35	0.62
1:H:152:ILE:N	1:H:153:ASP:CG	2.58	0.62
1:F:247:LEU:HD11	1:J:247:LEU:HB3	1.82	0.62
1:C:182:GLN:H	1:C:183:PRO:HD2	1.65	0.61
1:H:155:GLU:HB2	1:H:161:TRP:CD1	2.35	0.61
1:H:182:GLN:H	1:H:183:PRO:HD2	1.65	0.61
1:C:212:LEU:HD23	1:C:245:TYR:CD2	2.35	0.61
1:J:141:ARG:HG2	1:J:142:PHE:HD2	1.65	0.61
1:F:119:PHE:HB2	1:F:260:THR:HB	1.82	0.61
1:A:300:CYS:HB2	1:A:303:ALA:HB3	1.82	0.61
1:E:155:GLU:HB2	1:E:161:TRP:CD1	2.35	0.61
1:B:141:ARG:HG2	1:B:142:PHE:HD2	1.64	0.61
1:B:155:GLU:HB2	1:B:161:TRP:CD1	2.35	0.61
1:J:155:GLU:HB2	1:J:161:TRP:CD1	2.35	0.61
1:B:140:LEU:HD22	1:B:191:ILE:HD11	1.82	0.61
1:I:71:LEU:HD22	1:I:72:TRP:O	2.01	0.61
1:F:149:THR:HG22	1:F:153:ASP:OD2	2.01	0.60
1:B:289:ASN:ND2	1:B:292:GLU:HB3	2.15	0.60
1:C:141:ARG:HG2	1:C:142:PHE:HD2	1.65	0.60
1:F:165:LYS:HD3	1:F:166:ALA:H	1.65	0.60
1:E:150:GLU:HB2	1:E:153:ASP:OD2	2.00	0.60
1:G:168:THR:O	1:G:169:HIS:HB2	2.00	0.60
1:I:119:PHE:HB2	1:I:260:THR:HB	1.83	0.60
1:G:182:GLN:H	1:G:183:PRO:HD2	1.67	0.60
1:A:182:GLN:H	1:A:183:PRO:HD2	1.65	0.60
1:F:31:GLN:HG2	1:F:114:MET:HB2	1.84	0.60
1:F:260:THR:O	1:F:264:GLN:HG3	2.02	0.60
1:G:155:GLU:HB2	1:G:161:TRP:CD1	2.37	0.60
1:H:182:GLN:O	1:H:184:ASN:N	2.33	0.60
1:I:154:ASN:O	1:I:155:GLU:HB2	2.01	0.60
1:J:231:ARG:HB3	1:J:280:ILE:HD13	1.84	0.60
1:E:141:ARG:HG2	1:E:142:PHE:HD2	1.67	0.59
1:F:182:GLN:H	1:F:183:PRO:HD2	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:182:GLN:O	1:F:184:ASN:N	2.34	0.59
1:A:260:THR:O	1:A:264:GLN:HG3	2.01	0.59
1:G:140:LEU:HD13	1:G:191:ILE:CG1	2.32	0.59
1:A:141:ARG:HG2	1:A:142:PHE:HD2	1.68	0.59
1:A:155:GLU:HB2	1:A:161:TRP:CD1	2.38	0.59
1:I:154:ASN:O	1:I:155:GLU:CB	2.51	0.59
1:B:289:ASN:OD1	1:B:292:GLU:HB3	2.02	0.59
1:C:300:CYS:HB2	1:C:303:ALA:HB3	1.85	0.59
1:H:31:GLN:HG2	1:H:114:MET:HB2	1.85	0.59
1:I:182:GLN:H	1:I:183:PRO:HD2	1.68	0.59
1:D:182:GLN:H	1:D:183:PRO:HD2	1.68	0.59
1:D:119:PHE:HB2	1:D:260:THR:HB	1.85	0.59
1:F:76:LEU:HD12	1:F:76:LEU:H	1.68	0.59
1:H:150:GLU:HB3	1:H:153:ASP:CG	2.27	0.59
1:A:134:SER:OG	1:E:59:GLU:OE2	2.21	0.59
1:E:119:PHE:HB2	1:E:260:THR:HB	1.84	0.58
1:C:155:GLU:HB2	1:C:161:TRP:CD1	2.39	0.58
1:D:152:ILE:HA	1:D:155:GLU:CD	2.28	0.58
1:I:260:THR:O	1:I:264:GLN:HG3	2.03	0.58
1:A:215:ILE:HG12	1:B:239:MET:HE3	1.85	0.58
1:H:59:GLU:OE2	1:I:134:SER:OG	2.21	0.58
1:A:64:GLU:HG2	1:E:61:THR:HG21	1.86	0.58
1:D:31:GLN:HG2	1:D:114:MET:HB2	1.86	0.58
1:H:119:PHE:HB2	1:H:260:THR:HB	1.86	0.58
1:I:300:CYS:HB2	1:I:303:ALA:HB3	1.86	0.58
1:B:247:LEU:HB3	1:C:247:LEU:HD11	1.86	0.57
1:C:165:LYS:HD3	1:C:166:ALA:H	1.68	0.57
1:H:150:GLU:HB3	1:H:153:ASP:OD2	2.04	0.57
1:J:227:SER:O	1:J:231:ARG:HD3	2.04	0.57
1:B:168:THR:O	1:B:169:HIS:HB2	2.03	0.57
1:I:151:ASN:HB3	1:I:153:ASP:H	1.68	0.57
1:F:115:ASP:OD2	1:F:117:ARG:NH2	2.30	0.57
1:C:119:PHE:HB2	1:C:260:THR:HB	1.85	0.57
1:I:115:ASP:OD2	1:I:117:ARG:NH2	2.24	0.57
1:I:227:SER:O	1:I:231:ARG:HD3	2.04	0.57
1:A:182:GLN:O	1:A:184:ASN:N	2.35	0.57
1:C:91:ARG:CD	1:D:134:SER:HB3	2.32	0.57
1:H:141:ARG:HG2	1:H:142:PHE:HD2	1.70	0.57
1:I:151:ASN:O	1:I:155:GLU:OE2	2.22	0.57
1:D:155:GLU:HB2	1:D:161:TRP:CD1	2.40	0.57
1:H:114:MET:HG2	1:H:124:GLN:HE21	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:182:GLN:O	1:J:184:ASN:N	2.33	0.57
1:E:71:LEU:HD22	1:E:72:TRP:O	2.05	0.56
1:C:182:GLN:O	1:C:184:ASN:N	2.35	0.56
1:B:169:HIS:HE1	1:I:170:ILE:HD12	1.70	0.56
1:D:141:ARG:HG2	1:D:142:PHE:HD2	1.70	0.56
1:H:247:LEU:HB3	1:I:247:LEU:HD11	1.87	0.56
1:D:308:PHE:HA	1:D:311:ILE:HG12	1.86	0.56
1:F:134:SER:OG	1:J:59:GLU:OE2	2.22	0.56
1:F:249:THR:HG23	1:F:253:LEU:HD22	1.87	0.56
1:B:300:CYS:HB2	1:B:303:ALA:HB3	1.87	0.56
1:F:133:PHE:HE2	1:J:91:ARG:HB3	1.70	0.56
1:G:260:THR:O	1:G:264:GLN:HG3	2.06	0.56
1:B:182:GLN:H	1:B:183:PRO:HD2	1.69	0.56
1:B:263:ASP:O	1:B:267:ILE:HG13	2.06	0.56
1:I:151:ASN:CG	1:I:152:ILE:H	2.13	0.56
1:G:300:CYS:HB2	1:G:303:ALA:HB3	1.87	0.56
1:A:119:PHE:HB2	1:A:260:THR:HB	1.88	0.56
1:C:260:THR:O	1:C:264:GLN:HG3	2.06	0.56
1:C:284:HIS:CE1	1:C:291:VAL:HG12	2.38	0.56
1:F:239:MET:HE3	1:J:215:ILE:HG12	1.86	0.55
1:B:72:TRP:HZ3	1:B:135:TYR:CZ	2.24	0.55
1:G:91:ARG:CD	1:H:134:SER:HB3	2.35	0.55
1:E:284:HIS:CE1	1:E:291:VAL:HG12	2.38	0.55
1:A:263:ASP:O	1:A:267:ILE:HG13	2.06	0.55
1:C:72:TRP:HZ3	1:C:135:TYR:CZ	2.25	0.55
1:E:182:GLN:O	1:E:184:ASN:N	2.36	0.55
1:C:157:ILE:HD11	1:D:115:ASP:HB2	1.89	0.55
1:E:182:GLN:H	1:E:183:PRO:CD	2.20	0.55
1:I:145:ILE:HD13	1:I:166:ALA:HB3	1.87	0.55
1:J:182:GLN:H	1:J:183:PRO:CD	2.19	0.55
1:A:231:ARG:HB3	1:A:280:ILE:HD13	1.89	0.55
1:B:32:THR:HA	1:B:110:PHE:O	2.07	0.55
1:G:227:SER:O	1:G:231:ARG:HD3	2.06	0.55
1:H:76:LEU:HD12	1:H:76:LEU:H	1.71	0.55
1:I:72:TRP:HZ3	1:I:135:TYR:CZ	2.25	0.55
1:F:300:CYS:HB2	1:F:303:ALA:HB3	1.89	0.55
1:H:182:GLN:H	1:H:183:PRO:CD	2.20	0.55
1:C:231:ARG:HB3	1:C:280:ILE:HD13	1.88	0.54
1:F:114:MET:HG2	1:F:124:GLN:HE21	1.71	0.54
1:G:157:ILE:HD11	1:H:115:ASP:HB2	1.89	0.54
1:I:182:GLN:O	1:I:184:ASN:N	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:114:MET:HG2	1:J:124:GLN:HE21	1.72	0.54
1:J:300:CYS:HB2	1:J:303:ALA:HB3	1.88	0.54
1:G:249:THR:HG23	1:G:253:LEU:HD22	1.89	0.54
1:A:220:TRP:C	1:A:222:VAL:H	2.16	0.54
1:A:247:LEU:HB3	1:B:247:LEU:HD11	1.89	0.54
1:C:253:LEU:HG	1:C:254:PRO:HD2	1.89	0.54
1:F:141:ARG:HG2	1:F:142:PHE:HD2	1.72	0.54
1:H:227:SER:O	1:H:231:ARG:HD3	2.07	0.54
1:B:71:LEU:HD22	1:B:72:TRP:O	2.08	0.54
1:E:263:ASP:O	1:E:267:ILE:HG13	2.08	0.54
1:F:59:GLU:OE2	1:G:134:SER:OG	2.24	0.54
1:F:72:TRP:HZ3	1:F:135:TYR:CZ	2.26	0.54
1:I:299:ARG:HA	1:I:301:ARG:HG3	1.90	0.54
1:J:22:LYS:HE3	1:J:24:TYR:CD1	2.43	0.54
1:C:114:MET:HG2	1:C:124:GLN:HE21	1.73	0.54
1:H:212:LEU:O	1:H:216:ILE:HG12	2.07	0.54
1:H:224:TRP:HE3	1:I:281:ILE:HG12	1.72	0.54
1:J:173:ILE:HD12	1:J:174:ARG:H	1.73	0.54
1:D:182:GLN:O	1:D:184:ASN:N	2.38	0.54
1:G:247:LEU:HB3	1:H:247:LEU:HD11	1.89	0.54
1:G:119:PHE:HB2	1:G:260:THR:HB	1.89	0.53
1:B:76:LEU:HD12	1:B:76:LEU:H	1.73	0.53
1:B:215:ILE:HG12	1:C:239:MET:HE3	1.90	0.53
1:E:300:CYS:HB2	1:E:303:ALA:HB3	1.90	0.53
1:A:133:PHE:HE2	1:E:91:ARG:HB3	1.72	0.53
1:D:182:GLN:H	1:D:183:PRO:CD	2.21	0.53
1:G:263:ASP:O	1:G:267:ILE:HG13	2.08	0.53
1:D:263:ASP:O	1:D:267:ILE:HG13	2.09	0.53
1:I:147:VAL:HG12	1:I:149:THR:H	1.74	0.53
1:C:182:GLN:H	1:C:183:PRO:CD	2.20	0.53
1:I:94:LEU:HD23	1:I:100:VAL:HG22	1.89	0.53
1:B:260:THR:O	1:B:264:GLN:HG3	2.08	0.53
1:C:212:LEU:HD23	1:C:245:TYR:CE2	2.44	0.53
1:G:284:HIS:CE1	1:G:291:VAL:HG12	2.41	0.53
1:H:168:THR:HG22	1:H:169:HIS:H	1.73	0.53
1:B:231:ARG:HB3	1:B:280:ILE:HD13	1.91	0.53
1:D:257:PRO:HG2	1:D:258:TYR:CD2	2.44	0.53
1:E:72:TRP:HZ3	1:E:135:TYR:CZ	2.26	0.53
1:F:227:SER:O	1:F:231:ARG:HD3	2.09	0.53
1:I:114:MET:HG2	1:I:124:GLN:HE21	1.74	0.53
1:J:263:ASP:O	1:J:267:ILE:HG13	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:THR:HG23	1:B:253:LEU:HD22	1.91	0.53
1:D:260:THR:O	1:D:264:GLN:HG3	2.08	0.53
1:G:231:ARG:HB3	1:G:280:ILE:HD13	1.91	0.53
1:H:231:ARG:HB3	1:H:280:ILE:HD13	1.91	0.53
1:J:150:GLU:HB3	1:J:153:ASP:OD2	2.09	0.53
1:F:247:LEU:HB3	1:G:247:LEU:HD11	1.91	0.53
1:G:31:GLN:HG2	1:G:114:MET:HB2	1.90	0.53
1:H:263:ASP:O	1:H:267:ILE:HG13	2.09	0.53
1:D:165:LYS:HD3	1:D:166:ALA:N	2.24	0.52
1:D:289:ASN:O	1:D:289:ASN:ND2	2.39	0.52
1:D:300:CYS:HB2	1:D:303:ALA:HB3	1.91	0.52
1:F:257:PRO:HG2	1:F:258:TYR:CD2	2.44	0.52
1:G:225:LEU:HB2	1:G:231:ARG:HG3	1.90	0.52
1:J:220:TRP:C	1:J:222:VAL:H	2.17	0.52
1:A:182:GLN:H	1:A:183:PRO:CD	2.21	0.52
1:B:114:MET:HG2	1:B:124:GLN:HE21	1.74	0.52
1:J:260:THR:O	1:J:264:GLN:HG3	2.09	0.52
1:B:287:GLN:HB2	1:B:289:ASN:ND2	2.25	0.52
1:E:168:THR:HG22	1:E:169:HIS:H	1.73	0.52
1:I:284:HIS:CE1	1:I:291:VAL:HG12	2.39	0.52
1:A:76:LEU:HD12	1:A:76:LEU:H	1.74	0.52
1:D:94:LEU:HD23	1:D:100:VAL:HG22	1.91	0.52
1:D:140:LEU:HD12	1:D:189:SER:O	2.10	0.52
1:D:231:ARG:HB3	1:D:280:ILE:HD13	1.91	0.52
1:H:91:ARG:CD	1:I:134:SER:HB3	2.37	0.52
1:H:115:ASP:OD1	1:H:117:ARG:HB2	2.08	0.52
1:I:182:GLN:H	1:I:183:PRO:CD	2.23	0.52
1:E:212:LEU:HD23	1:E:245:TYR:CD2	2.45	0.52
1:E:227:SER:O	1:E:231:ARG:HD3	2.09	0.52
1:F:212:LEU:HD12	1:F:265:MET:SD	2.50	0.52
1:F:263:ASP:O	1:F:267:ILE:HG13	2.09	0.52
1:H:22:LYS:HE3	1:H:24:TYR:CD1	2.45	0.52
1:F:168:THR:HG22	1:F:169:HIS:H	1.74	0.52
1:A:312:GLY:HA2	1:A:315:LEU:HD12	1.91	0.52
1:B:182:GLN:O	1:B:184:ASN:N	2.41	0.52
1:C:71:LEU:HD22	1:C:72:TRP:O	2.10	0.52
1:C:224:TRP:HE3	1:D:281:ILE:HG12	1.74	0.52
1:D:212:LEU:HD23	1:D:245:TYR:CD2	2.45	0.52
1:H:220:TRP:C	1:H:222:VAL:H	2.18	0.52
1:A:224:TRP:HB2	1:B:281:ILE:HD11	1.91	0.52
1:D:71:LEU:HD22	1:D:72:TRP:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:140:LEU:HD13	1:B:191:ILE:CG1	2.33	0.52
1:I:154:ASN:ND2	1:I:154:ASN:N	2.55	0.52
1:J:257:PRO:HG2	1:J:258:TYR:CD2	2.44	0.52
1:G:257:PRO:HG2	1:G:258:TYR:CD2	2.45	0.51
1:J:168:THR:HG22	1:J:169:HIS:H	1.75	0.51
1:A:212:LEU:HD23	1:A:245:TYR:CD2	2.45	0.51
1:F:32:THR:HA	1:F:110:PHE:O	2.10	0.51
1:D:140:LEU:HD22	1:D:191:ILE:HD11	1.92	0.51
1:H:91:ARG:HB3	1:I:133:PHE:HE2	1.75	0.51
1:E:212:LEU:HD12	1:E:265:MET:SD	2.51	0.51
1:J:94:LEU:HD23	1:J:100:VAL:HG22	1.92	0.51
1:A:247:LEU:HD11	1:E:247:LEU:HB3	1.91	0.51
1:H:140:LEU:HD13	1:H:191:ILE:CG1	2.35	0.51
1:I:245:TYR:HD2	1:I:266:ILE:HD11	1.75	0.51
1:D:227:SER:O	1:D:231:ARG:HD3	2.11	0.51
1:G:72:TRP:HZ3	1:G:135:TYR:CZ	2.28	0.51
1:I:154:ASN:C	1:I:156:GLU:H	2.18	0.51
1:J:76:LEU:HD12	1:J:76:LEU:H	1.75	0.51
1:D:72:TRP:HZ3	1:D:135:TYR:CZ	2.29	0.51
1:A:72:TRP:HZ3	1:A:135:TYR:CZ	2.28	0.51
1:B:76:LEU:HD12	1:B:76:LEU:N	2.26	0.51
1:B:94:LEU:HD23	1:B:100:VAL:HG22	1.93	0.51
1:B:140:LEU:HD12	1:B:189:SER:O	2.10	0.51
1:B:174:ARG:NH1	1:I:13:ASP:OD2	2.43	0.51
1:B:287:GLN:NE2	1:B:290:GLY:O	2.43	0.51
1:C:310:ALA:C	1:C:312:GLY:H	2.16	0.51
1:G:212:LEU:O	1:G:216:ILE:HG12	2.10	0.51
1:H:72:TRP:HZ3	1:H:135:TYR:CZ	2.29	0.51
1:B:212:LEU:O	1:B:216:ILE:HG12	2.11	0.51
1:C:224:TRP:CE3	1:D:281:ILE:HG12	2.46	0.51
1:A:71:LEU:HD22	1:A:72:TRP:O	2.11	0.50
1:C:59:GLU:OE2	1:D:134:SER:OG	2.29	0.50
1:C:227:SER:O	1:C:231:ARG:HD3	2.11	0.50
1:H:115:ASP:OD2	1:H:117:ARG:NH2	2.30	0.50
1:J:316:VAL:HG23	1:J:317:ILE:H	1.76	0.50
1:A:212:LEU:O	1:A:216:ILE:HG12	2.11	0.50
1:E:289:ASN:OD1	1:E:290:GLY:N	2.44	0.50
1:I:210:LEU:HB3	1:I:211:PRO:HD3	1.93	0.50
1:B:220:TRP:C	1:B:222:VAL:H	2.17	0.50
1:F:182:GLN:H	1:F:183:PRO:CD	2.23	0.50
1:I:257:PRO:HG2	1:I:258:TYR:CD2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:64:GLU:HG2	1:J:61:THR:HG21	1.94	0.50
1:G:91:ARG:HB3	1:H:133:PHE:HE2	1.77	0.50
1:H:212:LEU:HD23	1:H:245:TYR:CD2	2.47	0.50
1:H:300:CYS:HB2	1:H:303:ALA:HB3	1.92	0.50
1:B:284:HIS:CE1	1:B:291:VAL:HG12	2.42	0.50
1:C:76:LEU:HD12	1:C:76:LEU:H	1.77	0.50
1:F:220:TRP:C	1:F:222:VAL:H	2.19	0.50
1:G:182:GLN:H	1:G:183:PRO:CD	2.23	0.50
1:J:72:TRP:HZ3	1:J:135:TYR:CZ	2.30	0.50
1:A:94:LEU:HD23	1:A:100:VAL:HG22	1.94	0.50
1:B:182:GLN:H	1:B:183:PRO:CD	2.24	0.50
1:G:299:ARG:HA	1:G:301:ARG:HG3	1.93	0.50
1:J:284:HIS:CE1	1:J:291:VAL:HG12	2.39	0.50
1:A:115:ASP:OD1	1:A:117:ARG:HB2	2.12	0.50
1:F:212:LEU:O	1:F:216:ILE:HG12	2.12	0.50
1:F:231:ARG:HB3	1:F:280:ILE:HD13	1.92	0.50
1:G:71:LEU:HD22	1:G:72:TRP:O	2.12	0.50
1:I:140:LEU:HD13	1:I:191:ILE:CG1	2.38	0.50
1:D:91:ARG:HB3	1:E:133:PHE:HE2	1.76	0.50
1:F:140:LEU:HD13	1:F:191:ILE:CG1	2.35	0.50
1:G:22:LYS:HE3	1:G:24:TYR:CD1	2.47	0.50
1:H:245:TYR:HD2	1:H:266:ILE:HD11	1.77	0.50
1:F:157:ILE:HD11	1:G:115:ASP:HB2	1.93	0.49
1:H:216:ILE:O	1:H:219:SER:HB3	2.12	0.49
1:I:115:ASP:OD1	1:I:117:ARG:HB2	2.12	0.49
1:I:147:VAL:C	1:I:149:THR:N	2.70	0.49
1:D:210:LEU:HB3	1:D:211:PRO:HD3	1.95	0.49
1:G:23:ILE:HG21	1:G:126:PHE:CD1	2.48	0.49
1:G:32:THR:HA	1:G:110:PHE:O	2.12	0.49
1:I:212:LEU:O	1:I:216:ILE:HG12	2.11	0.49
1:J:71:LEU:HD22	1:J:72:TRP:O	2.12	0.49
1:C:215:ILE:HG12	1:D:239:MET:HE3	1.94	0.49
1:C:287:GLN:NE2	1:C:290:GLY:O	2.45	0.49
1:F:168:THR:O	1:F:169:HIS:HB2	2.11	0.49
1:F:224:TRP:HE3	1:G:281:ILE:HG12	1.77	0.49
1:G:245:TYR:HD2	1:G:266:ILE:HD11	1.78	0.49
1:I:76:LEU:H	1:I:76:LEU:HD12	1.76	0.49
1:C:263:ASP:O	1:C:267:ILE:HG13	2.13	0.49
1:D:115:ASP:OD2	1:D:117:ARG:NH2	2.33	0.49
1:E:115:ASP:OD1	1:E:117:ARG:HB2	2.11	0.49
1:G:115:ASP:OD1	1:G:117:ARG:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:212:LEU:O	1:J:216:ILE:HG12	2.12	0.49
1:B:163:ARG:NH1	1:I:151:ASN:CG	2.69	0.49
1:C:168:THR:O	1:C:169:HIS:HB2	2.12	0.49
1:D:245:TYR:HD2	1:D:266:ILE:HD11	1.78	0.49
1:H:289:ASN:OD1	1:H:290:GLY:N	2.45	0.49
1:J:249:THR:HG23	1:J:253:LEU:HD22	1.94	0.49
1:C:72:TRP:CD1	1:C:72:TRP:C	2.90	0.49
1:D:299:ARG:HA	1:D:301:ARG:HG3	1.93	0.49
1:G:140:LEU:HD22	1:G:191:ILE:HD11	1.95	0.49
1:G:212:LEU:HD12	1:G:265:MET:SD	2.52	0.49
1:A:114:MET:HG2	1:A:124:GLN:HE21	1.78	0.49
1:A:178:LEU:HD23	1:A:186:ASN:HD22	1.77	0.49
1:D:247:LEU:HB3	1:E:247:LEU:HD11	1.93	0.49
1:F:212:LEU:HD23	1:F:245:TYR:CD2	2.47	0.49
1:I:32:THR:HA	1:I:110:PHE:O	2.13	0.49
1:A:204:TYR:O	1:A:209:ILE:HG12	2.13	0.49
1:F:71:LEU:HD22	1:F:72:TRP:O	2.13	0.49
1:H:224:TRP:CE3	1:I:281:ILE:HG12	2.47	0.49
1:H:260:THR:O	1:H:264:GLN:HG3	2.13	0.49
1:I:263:ASP:O	1:I:267:ILE:HG13	2.13	0.49
1:J:23:ILE:HG21	1:J:126:PHE:CD1	2.48	0.49
1:G:168:THR:HG22	1:G:169:HIS:H	1.77	0.49
1:G:204:TYR:O	1:G:209:ILE:HG12	2.13	0.49
1:H:71:LEU:HD22	1:H:72:TRP:O	2.13	0.49
1:H:204:TYR:O	1:H:209:ILE:HG12	2.13	0.49
1:I:150:GLU:OE1	1:I:154:ASN:ND2	2.46	0.49
1:I:249:THR:HG23	1:I:253:LEU:HD22	1.93	0.49
1:B:22:LYS:HE3	1:B:24:TYR:CD1	2.48	0.49
1:B:155:GLU:H	1:B:155:GLU:HG3	1.42	0.49
1:I:220:TRP:C	1:I:222:VAL:H	2.21	0.49
1:I:313:CYS:O	1:I:316:VAL:HG22	2.13	0.49
1:J:168:THR:O	1:J:169:HIS:HB2	2.12	0.49
1:C:249:THR:HG23	1:C:253:LEU:HD22	1.94	0.48
1:E:168:THR:O	1:E:169:HIS:HB2	2.13	0.48
1:E:225:LEU:HB2	1:E:231:ARG:HG3	1.95	0.48
1:E:231:ARG:HB3	1:E:280:ILE:HD13	1.95	0.48
1:A:287:GLN:NE2	1:A:290:GLY:O	2.46	0.48
1:B:224:TRP:HE3	1:C:281:ILE:HG12	1.77	0.48
1:F:224:TRP:CE3	1:G:281:ILE:HG12	2.48	0.48
1:A:22:LYS:HE3	1:A:24:TYR:CD1	2.48	0.48
1:B:91:ARG:HB3	1:C:133:PHE:HE2	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:220:TRP:C	1:C:222:VAL:H	2.22	0.48
1:E:249:THR:HG23	1:E:253:LEU:HD22	1.96	0.48
1:H:76:LEU:HD12	1:H:76:LEU:N	2.28	0.48
1:B:257:PRO:HG2	1:B:258:TYR:CD2	2.48	0.48
1:D:212:LEU:O	1:D:216:ILE:HG12	2.14	0.48
1:E:212:LEU:O	1:E:216:ILE:HG12	2.13	0.48
1:F:284:HIS:CE1	1:F:291:VAL:HG12	2.41	0.48
1:I:287:GLN:NE2	1:I:290:GLY:O	2.47	0.48
1:B:163:ARG:HH11	1:I:151:ASN:CG	2.22	0.48
1:C:155:GLU:H	1:C:155:GLU:HG3	1.43	0.48
1:E:162:ILE:H	1:E:162:ILE:HG12	1.42	0.48
1:A:210:LEU:HB3	1:A:211:PRO:HD3	1.95	0.48
1:C:247:LEU:HB3	1:D:247:LEU:HD11	1.95	0.48
1:D:72:TRP:CD1	1:D:72:TRP:C	2.92	0.48
1:E:220:TRP:C	1:E:222:VAL:H	2.22	0.48
1:H:32:THR:HA	1:H:110:PHE:O	2.14	0.48
1:I:216:ILE:O	1:I:219:SER:HB3	2.14	0.48
1:F:76:LEU:HD12	1:F:76:LEU:N	2.28	0.48
1:A:157:ILE:HD11	1:B:115:ASP:HB2	1.94	0.47
1:B:227:SER:O	1:B:231:ARG:HD3	2.12	0.47
1:H:168:THR:O	1:H:169:HIS:HB2	2.14	0.47
1:H:284:HIS:CE1	1:H:291:VAL:HG12	2.49	0.47
1:C:72:TRP:CZ3	1:C:135:TYR:CZ	3.02	0.47
1:D:162:ILE:H	1:D:162:ILE:HG12	1.37	0.47
1:B:204:TYR:O	1:B:209:ILE:HG12	2.14	0.47
1:C:67:ILE:HG12	1:C:73:VAL:HG23	1.95	0.47
1:D:59:GLU:OE2	1:E:134:SER:OG	2.31	0.47
1:D:287:GLN:NE2	1:D:290:GLY:O	2.47	0.47
1:I:165:LYS:HD3	1:I:166:ALA:N	2.27	0.47
1:C:56:LEU:HD22	1:C:56:LEU:HA	1.73	0.47
1:C:245:TYR:HD2	1:C:266:ILE:HD11	1.79	0.47
1:C:257:PRO:HG2	1:C:258:TYR:CD2	2.49	0.47
1:E:22:LYS:HE3	1:E:24:TYR:CD1	2.50	0.47
1:E:210:LEU:HB3	1:E:211:PRO:HD3	1.97	0.47
1:E:257:PRO:HG2	1:E:258:TYR:CD2	2.48	0.47
1:E:299:ARG:HA	1:E:301:ARG:HG3	1.97	0.47
1:J:119:PHE:CB	1:J:260:THR:HB	2.44	0.47
1:C:32:THR:HA	1:C:110:PHE:O	2.15	0.47
1:F:162:ILE:H	1:F:162:ILE:HG12	1.40	0.47
1:G:220:TRP:C	1:G:222:VAL:H	2.22	0.47
1:A:168:THR:O	1:A:169:HIS:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:LYS:HD3	1:B:166:ALA:N	2.26	0.47
1:B:168:THR:HG22	1:B:169:HIS:H	1.80	0.47
1:F:22:LYS:HE3	1:F:24:TYR:CD1	2.50	0.47
1:F:253:LEU:HG	1:F:254:PRO:HD2	1.95	0.47
1:G:224:TRP:HB2	1:H:281:ILE:HD11	1.97	0.47
1:B:107:LEU:HB3	1:C:83:GLY:HA2	1.96	0.47
1:B:145:ILE:HG21	1:B:193:VAL:HG11	1.95	0.47
1:B:224:TRP:CE3	1:C:281:ILE:HG12	2.50	0.47
1:B:295:LEU:HA	1:B:298:GLN:NE2	2.30	0.47
1:G:76:LEU:HD12	1:G:76:LEU:H	1.78	0.47
1:I:22:LYS:HE3	1:I:24:TYR:CD1	2.50	0.47
1:I:152:ILE:O	1:I:153:ASP:C	2.57	0.47
1:I:168:THR:O	1:I:169:HIS:HB2	2.15	0.47
1:A:253:LEU:HG	1:A:254:PRO:HD2	1.96	0.47
1:H:92:LEU:HD23	1:H:92:LEU:HA	1.61	0.47
1:I:92:LEU:HD23	1:I:92:LEU:HA	1.67	0.47
1:J:67:ILE:HG12	1:J:73:VAL:HG23	1.96	0.47
1:J:130:LEU:HD23	1:J:130:LEU:HA	1.76	0.47
1:A:92:LEU:HD23	1:A:92:LEU:HA	1.57	0.47
1:D:204:TYR:O	1:D:209:ILE:HG12	2.14	0.47
1:E:23:ILE:HG21	1:E:126:PHE:CD1	2.50	0.47
1:A:134:SER:HB3	1:E:91:ARG:CD	2.41	0.47
1:B:72:TRP:CZ3	1:B:135:TYR:CZ	3.03	0.47
1:D:91:ARG:CD	1:E:134:SER:HB3	2.41	0.47
1:B:299:ARG:HA	1:B:301:ARG:HG3	1.97	0.46
1:F:115:ASP:OD1	1:F:117:ARG:HB2	2.15	0.46
1:G:59:GLU:OE2	1:H:134:SER:OG	2.32	0.46
1:G:94:LEU:HD23	1:G:100:VAL:HG22	1.95	0.46
1:A:299:ARG:HA	1:A:301:ARG:HG3	1.97	0.46
1:F:91:ARG:CD	1:G:134:SER:HB3	2.40	0.46
1:F:295:LEU:HA	1:F:298:GLN:NE2	2.30	0.46
1:F:299:ARG:HA	1:F:301:ARG:HG3	1.97	0.46
1:J:210:LEU:HB3	1:J:211:PRO:HD3	1.98	0.46
1:B:224:TRP:HB2	1:C:281:ILE:HD11	1.96	0.46
1:C:299:ARG:HA	1:C:301:ARG:HG3	1.98	0.46
1:I:72:TRP:CZ3	1:I:135:TYR:CZ	3.04	0.46
1:D:22:LYS:HE3	1:D:24:TYR:CD1	2.49	0.46
1:D:224:TRP:HB2	1:E:281:ILE:HD11	1.98	0.46
1:F:155:GLU:H	1:F:155:GLU:HG3	1.44	0.46
1:H:21:ASN:HB2	1:H:36:ASP:O	2.15	0.46
1:H:287:GLN:NE2	1:H:290:GLY:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:299:ARG:HA	1:J:301:ARG:HG3	1.96	0.46
1:B:157:ILE:HD11	1:C:115:ASP:HB2	1.96	0.46
1:D:212:LEU:HD12	1:D:265:MET:SD	2.55	0.46
1:F:215:ILE:HG12	1:G:239:MET:HE3	1.97	0.46
1:D:76:LEU:H	1:D:76:LEU:HD12	1.81	0.46
1:H:257:PRO:HG2	1:H:258:TYR:CD2	2.50	0.46
1:I:255:ARG:O	1:I:256:LEU:HD23	2.16	0.46
1:J:212:LEU:HD23	1:J:245:TYR:CD2	2.51	0.46
1:A:24:TYR:CE2	1:A:34:LYS:HD2	2.51	0.46
1:D:115:ASP:OD1	1:D:117:ARG:HB2	2.16	0.46
1:E:287:GLN:NE2	1:E:290:GLY:O	2.48	0.46
1:G:155:GLU:H	1:G:155:GLU:HG3	1.42	0.46
1:G:252:ILE:HD13	1:G:252:ILE:HA	1.78	0.46
1:I:72:TRP:CD1	1:I:72:TRP:C	2.94	0.46
1:J:115:ASP:OD2	1:J:117:ARG:NH2	2.37	0.46
1:J:145:ILE:HG21	1:J:193:VAL:HG11	1.98	0.46
1:A:173:ILE:HD12	1:A:174:ARG:H	1.81	0.46
1:D:178:LEU:HD23	1:D:186:ASN:HD22	1.80	0.46
1:G:307:GLY:O	1:G:311:ILE:HD12	2.15	0.46
1:J:204:TYR:O	1:J:209:ILE:HG12	2.15	0.46
1:A:91:ARG:CD	1:B:134:SER:HB3	2.42	0.46
1:D:220:TRP:C	1:D:222:VAL:H	2.24	0.46
1:F:204:TYR:O	1:F:209:ILE:HG12	2.15	0.46
1:B:162:ILE:H	1:B:162:ILE:HG12	1.43	0.46
1:E:140:LEU:HD13	1:E:191:ILE:CG1	2.42	0.46
1:G:260:THR:H	1:G:263:ASP:HB2	1.81	0.46
1:H:157:ILE:HD11	1:I:115:ASP:HB2	1.97	0.46
1:A:59:GLU:OE2	1:B:134:SER:OG	2.33	0.45
1:B:91:ARG:CD	1:C:134:SER:HB3	2.36	0.45
1:B:225:LEU:HB2	1:B:231:ARG:HG3	1.98	0.45
1:D:32:THR:HA	1:D:110:PHE:O	2.16	0.45
1:E:204:TYR:O	1:E:209:ILE:HG12	2.15	0.45
1:H:151:ASN:CA	1:H:153:ASP:OD2	2.63	0.45
1:H:205:LEU:HD23	1:H:205:LEU:HA	1.76	0.45
1:A:23:ILE:HG21	1:A:126:PHE:CD1	2.52	0.45
1:A:257:PRO:HG2	1:A:258:TYR:CD2	2.51	0.45
1:C:22:LYS:HE3	1:C:24:TYR:CD1	2.51	0.45
1:C:130:LEU:HD23	1:C:130:LEU:HA	1.85	0.45
1:I:225:LEU:HB2	1:I:231:ARG:HG3	1.98	0.45
1:B:151:ASN:O	1:B:155:GLU:HG2	2.17	0.45
1:E:143:SER:HB3	1:E:168:THR:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:255:ARG:O	1:F:256:LEU:HD23	2.17	0.45
1:G:131:GLU:HA	1:G:132:PRO:HD2	1.64	0.45
1:C:212:LEU:O	1:C:216:ILE:HG12	2.16	0.45
1:G:92:LEU:HD23	1:G:92:LEU:HA	1.68	0.45
1:H:210:LEU:HB3	1:H:211:PRO:HD3	1.97	0.45
1:I:145:ILE:HG21	1:I:193:VAL:HG11	1.99	0.45
1:A:91:ARG:HB3	1:B:133:PHE:HE2	1.81	0.45
1:A:226:GLU:OE2	1:B:284:HIS:NE2	2.30	0.45
1:B:210:LEU:HB3	1:B:211:PRO:HD3	1.99	0.45
1:H:140:LEU:HD22	1:H:191:ILE:HD11	1.98	0.45
1:I:178:LEU:HD23	1:I:186:ASN:HD22	1.81	0.45
1:A:83:GLY:HA2	1:E:107:LEU:HB3	1.99	0.45
1:D:118:LEU:H	1:D:118:LEU:HG	1.46	0.45
1:D:247:LEU:HD22	1:E:247:LEU:HD11	1.98	0.45
1:A:95:PHE:HE1	1:A:101:ILE:HD12	1.81	0.45
1:A:168:THR:HG22	1:A:169:HIS:H	1.81	0.45
1:B:252:ILE:HD13	1:B:252:ILE:HA	1.81	0.45
1:D:260:THR:H	1:D:263:ASP:HB2	1.82	0.45
1:F:281:ILE:HG12	1:J:224:TRP:HE3	1.81	0.45
1:G:67:ILE:HG12	1:G:73:VAL:HG23	1.99	0.45
1:A:224:TRP:CE3	1:B:281:ILE:HG12	2.51	0.45
1:B:212:LEU:HD12	1:B:265:MET:SD	2.57	0.45
1:D:216:ILE:O	1:D:219:SER:HB3	2.17	0.45
1:E:264:GLN:O	1:E:267:ILE:N	2.48	0.45
1:H:123:ARG:HE	1:H:123:ARG:HB3	1.51	0.45
1:I:118:LEU:H	1:I:118:LEU:HG	1.46	0.45
1:C:95:PHE:HE1	1:C:101:ILE:HD12	1.82	0.45
1:E:246:ALA:O	1:E:249:THR:HB	2.17	0.45
1:F:178:LEU:HD23	1:F:186:ASN:HD22	1.82	0.45
1:G:182:GLN:O	1:G:184:ASN:N	2.41	0.45
1:H:260:THR:H	1:H:263:ASP:HB2	1.81	0.45
1:A:130:LEU:HD23	1:A:130:LEU:HA	1.81	0.45
1:D:56:LEU:HD22	1:D:56:LEU:HA	1.70	0.45
1:G:140:LEU:HD13	1:G:191:ILE:CD1	2.47	0.45
1:C:76:LEU:HD12	1:C:76:LEU:N	2.32	0.44
1:J:131:GLU:HA	1:J:132:PRO:HD2	1.63	0.44
1:E:165:LYS:HD3	1:E:166:ALA:N	2.31	0.44
1:F:153:ASP:HB3	1:F:154:ASN:H	1.51	0.44
1:F:173:ILE:HD12	1:F:174:ARG:H	1.82	0.44
1:F:212:LEU:HD23	1:F:245:TYR:CE2	2.52	0.44
1:I:130:LEU:HD23	1:I:130:LEU:HA	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:231:ARG:HB3	1:I:280:ILE:HD13	1.98	0.44
1:J:115:ASP:OD1	1:J:117:ARG:HB2	2.18	0.44
1:D:72:TRP:CZ3	1:D:135:TYR:CZ	3.06	0.44
1:F:95:PHE:HE1	1:F:101:ILE:HD12	1.82	0.44
1:C:162:ILE:H	1:C:162:ILE:HG12	1.38	0.44
1:G:165:LYS:HD3	1:G:166:ALA:N	2.30	0.44
1:G:216:ILE:O	1:G:219:SER:HB3	2.18	0.44
1:H:256:LEU:HD13	1:H:258:TYR:CE1	2.53	0.44
1:B:264:GLN:O	1:B:267:ILE:N	2.49	0.44
1:C:168:THR:HG22	1:C:169:HIS:H	1.82	0.44
1:D:153:ASP:HB3	1:D:154:ASN:H	1.49	0.44
1:F:92:LEU:HD23	1:F:92:LEU:HA	1.69	0.44
1:J:118:LEU:H	1:J:118:LEU:HG	1.48	0.44
1:D:131:GLU:HA	1:D:132:PRO:HD2	1.61	0.44
1:G:255:ARG:O	1:G:256:LEU:HD23	2.17	0.44
1:H:24:TYR:CE2	1:H:34:LYS:HD2	2.53	0.44
1:H:284:HIS:HE1	1:H:291:VAL:HG12	1.81	0.44
1:I:152:ILE:O	1:I:154:ASN:N	2.50	0.44
1:A:131:GLU:HA	1:A:132:PRO:HD2	1.66	0.44
1:A:227:SER:O	1:A:231:ARG:HD3	2.18	0.44
1:A:284:HIS:CE1	1:A:291:VAL:HG12	2.42	0.44
1:D:212:LEU:HD23	1:D:245:TYR:CE2	2.53	0.44
1:G:205:LEU:HD23	1:G:205:LEU:HA	1.76	0.44
1:J:140:LEU:HD12	1:J:189:SER:O	2.17	0.44
1:D:165:LYS:CD	1:D:166:ALA:H	2.27	0.44
1:I:140:LEU:HD12	1:I:189:SER:O	2.18	0.44
1:I:143:SER:N	1:I:170:ILE:HD11	2.33	0.44
1:I:212:LEU:HD23	1:I:245:TYR:CD2	2.52	0.44
1:A:123:ARG:HE	1:A:123:ARG:HB3	1.54	0.44
1:A:245:TYR:HD2	1:A:266:ILE:HD11	1.83	0.44
1:B:178:LEU:HD23	1:B:186:ASN:HD22	1.83	0.44
1:C:72:TRP:O	1:C:72:TRP:CD1	2.71	0.44
1:E:72:TRP:CZ3	1:E:135:TYR:CZ	3.06	0.44
1:G:178:LEU:HD23	1:G:186:ASN:HD22	1.83	0.44
1:H:255:ARG:O	1:H:256:LEU:HD23	2.18	0.44
1:J:76:LEU:HD12	1:J:76:LEU:N	2.33	0.44
1:A:165:LYS:HD3	1:A:166:ALA:N	2.32	0.43
1:C:287:GLN:HB2	1:C:288:ALA:H	1.53	0.43
1:E:32:THR:HA	1:E:110:PHE:O	2.18	0.43
1:G:202:SER:OG	1:G:203:TYR:N	2.49	0.43
1:A:42:GLN:HA	1:A:100:VAL:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:ASP:OD1	1:B:117:ARG:HB2	2.17	0.43
1:D:249:THR:HG23	1:D:253:LEU:HD22	2.00	0.43
1:G:72:TRP:CZ3	1:G:135:TYR:CZ	3.06	0.43
1:I:173:ILE:HD12	1:I:173:ILE:HA	1.86	0.43
1:J:95:PHE:HE1	1:J:101:ILE:HD12	1.83	0.43
1:B:72:TRP:CD1	1:B:72:TRP:C	2.97	0.43
1:B:131:GLU:HA	1:B:132:PRO:HD2	1.68	0.43
1:G:72:TRP:CD1	1:G:72:TRP:C	2.96	0.43
1:F:72:TRP:CZ3	1:F:135:TYR:CZ	3.06	0.43
1:G:212:LEU:HD23	1:G:245:TYR:CD2	2.53	0.43
1:H:94:LEU:HD23	1:H:100:VAL:HG22	2.00	0.43
1:I:143:SER:HB3	1:I:168:THR:HG21	2.00	0.43
1:J:252:ILE:HD13	1:J:252:ILE:HA	1.82	0.43
1:J:295:LEU:HA	1:J:298:GLN:NE2	2.34	0.43
1:F:224:TRP:HB2	1:G:281:ILE:HD11	2.01	0.43
1:G:140:LEU:HD12	1:G:189:SER:O	2.18	0.43
1:H:299:ARG:HA	1:H:301:ARG:HG3	2.00	0.43
1:I:174:ARG:HA	1:I:186:ASN:O	2.19	0.43
1:A:212:LEU:HD23	1:A:245:TYR:CE2	2.54	0.43
1:F:281:ILE:HG12	1:J:224:TRP:CE3	2.53	0.43
1:I:147:VAL:C	1:I:149:THR:H	2.27	0.43
1:B:119:PHE:CB	1:B:260:THR:HB	2.45	0.43
1:C:228:PHE:CZ	1:C:232:LEU:HD12	2.53	0.43
1:E:130:LEU:HD23	1:E:130:LEU:HA	1.83	0.43
1:F:210:LEU:HB3	1:F:211:PRO:HD3	2.01	0.43
1:I:205:LEU:HD23	1:I:205:LEU:HA	1.76	0.43
1:D:119:PHE:CB	1:D:260:THR:HB	2.47	0.43
1:D:145:ILE:HD13	1:D:166:ALA:HB3	2.00	0.43
1:D:253:LEU:HG	1:D:254:PRO:HD2	2.00	0.43
1:E:119:PHE:CB	1:E:260:THR:HB	2.48	0.43
1:F:91:ARG:HB3	1:G:133:PHE:HE2	1.84	0.43
1:H:284:HIS:HD2	1:H:285:HIS:NE2	2.17	0.43
1:J:56:LEU:HD22	1:J:56:LEU:HA	1.64	0.43
1:C:91:ARG:HB3	1:D:133:PHE:HE2	1.83	0.43
1:F:94:LEU:HD23	1:F:100:VAL:HG22	2.01	0.43
1:F:145:ILE:HG21	1:F:193:VAL:HG11	1.99	0.43
1:G:56:LEU:HD22	1:G:56:LEU:HA	1.67	0.43
1:H:155:GLU:H	1:H:155:GLU:HG3	1.42	0.43
1:I:204:TYR:O	1:I:209:ILE:HG12	2.18	0.43
1:J:225:LEU:HB2	1:J:231:ARG:HG3	2.00	0.43
1:F:23:ILE:HG21	1:F:126:PHE:CD1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:SER:N	1:A:170:ILE:HD11	2.34	0.42
1:A:224:TRP:HE3	1:B:281:ILE:HG12	1.83	0.42
1:B:253:LEU:HG	1:B:254:PRO:HD2	2.00	0.42
1:B:308:PHE:C	1:B:310:ALA:H	2.26	0.42
1:C:24:TYR:CE2	1:C:34:LYS:HD2	2.54	0.42
1:D:168:THR:HG22	1:D:169:HIS:H	1.83	0.42
1:E:173:ILE:HD12	1:E:174:ARG:H	1.83	0.42
1:J:264:GLN:O	1:J:267:ILE:N	2.51	0.42
1:B:115:ASP:OD2	1:B:117:ARG:NH2	2.35	0.42
1:B:245:TYR:HD2	1:B:266:ILE:HD11	1.84	0.42
1:H:143:SER:HB3	1:H:168:THR:HG21	2.01	0.42
1:H:162:ILE:H	1:H:162:ILE:HG12	1.40	0.42
1:I:245:TYR:CD2	1:I:266:ILE:HD11	2.54	0.42
1:C:40:VAL:HA	1:C:102:TYR:O	2.19	0.42
1:C:140:LEU:HD13	1:C:191:ILE:CG1	2.40	0.42
1:E:205:LEU:HD23	1:E:205:LEU:HA	1.78	0.42
1:F:118:LEU:H	1:F:118:LEU:HG	1.46	0.42
1:G:287:GLN:NE2	1:G:290:GLY:O	2.52	0.42
1:G:308:PHE:C	1:G:310:ALA:H	2.27	0.42
1:H:118:LEU:H	1:H:118:LEU:HG	1.44	0.42
1:H:252:ILE:HD13	1:H:252:ILE:HA	1.72	0.42
1:H:310:ALA:C	1:H:312:GLY:H	2.27	0.42
1:I:140:LEU:HD22	1:I:191:ILE:HD11	2.01	0.42
1:A:72:TRP:CZ3	1:A:135:TYR:CZ	3.07	0.42
1:A:132:PRO:HD2	1:A:189:SER:O	2.20	0.42
1:A:145:ILE:HD12	1:A:145:ILE:H	1.84	0.42
1:A:264:GLN:O	1:A:267:ILE:N	2.52	0.42
1:C:178:LEU:HD23	1:C:186:ASN:HD22	1.84	0.42
1:C:225:LEU:HB2	1:C:231:ARG:HG3	2.02	0.42
1:E:173:ILE:HD12	1:E:173:ILE:HA	1.86	0.42
1:G:130:LEU:HD23	1:G:130:LEU:HA	1.74	0.42
1:G:253:LEU:HG	1:G:254:PRO:HD2	2.01	0.42
1:I:76:LEU:HD12	1:I:76:LEU:N	2.34	0.42
1:J:92:LEU:HD23	1:J:92:LEU:HA	1.68	0.42
1:A:76:LEU:HD12	1:A:76:LEU:N	2.34	0.42
1:A:220:TRP:C	1:A:222:VAL:N	2.78	0.42
1:A:225:LEU:HB2	1:A:231:ARG:HG3	2.01	0.42
1:D:165:LYS:HD3	1:D:165:LYS:HA	1.77	0.42
1:F:119:PHE:CB	1:F:260:THR:HB	2.49	0.42
1:G:24:TYR:CE2	1:G:34:LYS:HD2	2.54	0.42
1:G:264:GLN:O	1:G:267:ILE:N	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:72:TRP:CZ3	1:H:135:TYR:CZ	3.07	0.42
1:H:278:LEU:HD23	1:H:278:LEU:HA	1.87	0.42
1:J:205:LEU:HD23	1:J:205:LEU:HA	1.79	0.42
1:A:239:MET:HE3	1:E:215:ILE:HG12	2.00	0.42
1:C:118:LEU:H	1:C:118:LEU:HG	1.47	0.42
1:D:92:LEU:HD23	1:D:92:LEU:HA	1.69	0.42
1:D:151:ASN:O	1:D:155:GLU:HG2	2.20	0.42
1:E:212:LEU:HD23	1:E:245:TYR:CE2	2.55	0.42
1:H:23:ILE:HG21	1:H:126:PHE:CD1	2.55	0.42
1:H:178:LEU:HB2	1:H:179:SER:H	1.74	0.42
1:I:131:GLU:HA	1:I:132:PRO:HD2	1.66	0.42
1:I:165:LYS:CD	1:I:166:ALA:H	2.29	0.42
1:J:245:TYR:HD2	1:J:266:ILE:HD11	1.84	0.42
1:C:224:TRP:HB2	1:D:281:ILE:HD11	2.01	0.42
1:F:131:GLU:HA	1:F:132:PRO:HD2	1.66	0.42
1:I:253:LEU:HG	1:I:254:PRO:HD2	2.01	0.42
1:A:308:PHE:C	1:A:310:ALA:H	2.27	0.42
1:D:295:LEU:HA	1:D:298:GLN:NE2	2.34	0.42
1:E:115:ASP:OD2	1:E:117:ARG:NH2	2.37	0.42
1:E:178:LEU:HD23	1:E:186:ASN:HD22	1.83	0.42
1:F:216:ILE:O	1:F:219:SER:HB3	2.19	0.42
1:A:205:LEU:HD23	1:A:205:LEU:HA	1.77	0.42
1:B:169:HIS:CE1	1:I:168:THR:HB	2.53	0.42
1:C:92:LEU:HD23	1:C:92:LEU:HA	1.64	0.42
1:D:168:THR:O	1:D:169:HIS:HB2	2.19	0.42
1:G:76:LEU:HD12	1:G:76:LEU:N	2.35	0.42
1:G:178:LEU:HB2	1:G:179:SER:H	1.75	0.42
1:B:179:SER:HB3	1:B:180:SER:H	1.67	0.42
1:D:225:LEU:HB2	1:D:231:ARG:HG3	2.02	0.42
1:E:94:LEU:HD23	1:E:100:VAL:HG22	2.01	0.42
1:E:143:SER:N	1:E:170:ILE:HD11	2.35	0.42
1:F:143:SER:N	1:F:170:ILE:HD11	2.35	0.42
1:F:278:LEU:HD23	1:F:278:LEU:HA	1.88	0.42
1:G:163:ARG:N	1:G:164:GLY:HA3	2.35	0.42
1:A:24:TYR:C	1:A:24:TYR:CD2	2.97	0.41
1:F:245:TYR:HD2	1:F:266:ILE:HD11	1.85	0.41
1:I:23:ILE:HG21	1:I:126:PHE:CD1	2.54	0.41
1:I:168:THR:HG22	1:I:169:HIS:H	1.84	0.41
1:I:295:LEU:HA	1:I:298:GLN:NE2	2.35	0.41
1:A:252:ILE:HD13	1:A:252:ILE:HA	1.82	0.41
1:C:173:ILE:HD12	1:C:174:ARG:H	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:76:LEU:HD12	1:E:76:LEU:H	1.85	0.41
1:E:145:ILE:HD13	1:E:166:ALA:HB3	2.02	0.41
1:J:238:LEU:HD12	1:J:238:LEU:HA	1.83	0.41
1:B:23:ILE:HG21	1:B:126:PHE:CD1	2.56	0.41
1:C:23:ILE:HG21	1:C:126:PHE:CD1	2.55	0.41
1:D:173:ILE:HD12	1:D:174:ARG:H	1.86	0.41
1:G:256:LEU:HD23	1:G:256:LEU:HA	1.82	0.41
1:I:157:ILE:HD11	1:J:115:ASP:HB2	2.02	0.41
1:J:123:ARG:HE	1:J:123:ARG:HB3	1.51	0.41
1:C:278:LEU:HD23	1:C:278:LEU:HA	1.87	0.41
1:D:310:ALA:O	1:D:314:VAL:HG23	2.20	0.41
1:E:253:LEU:HG	1:E:254:PRO:HD2	2.02	0.41
1:E:255:ARG:O	1:E:256:LEU:HD23	2.21	0.41
1:G:40:VAL:HA	1:G:102:TYR:O	2.20	0.41
1:H:72:TRP:CD1	1:H:72:TRP:C	2.98	0.41
1:I:150:GLU:HG3	1:I:151:ASN:H	1.85	0.41
1:B:67:ILE:HG12	1:B:73:VAL:HG23	2.01	0.41
1:B:165:LYS:HD3	1:B:165:LYS:HA	1.81	0.41
1:D:216:ILE:HD13	1:D:216:ILE:HA	1.83	0.41
1:E:216:ILE:O	1:E:219:SER:HB3	2.20	0.41
1:I:252:ILE:HA	1:I:252:ILE:HD13	1.80	0.41
1:J:143:SER:N	1:J:170:ILE:HD11	2.35	0.41
1:A:153:ASP:HB3	1:A:154:ASN:H	1.52	0.41
1:B:59:GLU:OE2	1:C:134:SER:OG	2.39	0.41
1:E:278:LEU:HD23	1:E:278:LEU:HA	1.93	0.41
1:H:28:THR:HA	1:H:116:PHE:CE1	2.56	0.41
1:H:119:PHE:CB	1:H:260:THR:HB	2.49	0.41
1:H:227:SER:HB3	1:H:230:GLU:CD	2.46	0.41
1:B:220:TRP:C	1:B:222:VAL:N	2.79	0.41
1:D:40:VAL:HA	1:D:102:TYR:O	2.20	0.41
1:F:252:ILE:HD13	1:F:252:ILE:HA	1.84	0.41
1:G:162:ILE:H	1:G:162:ILE:HG12	1.41	0.41
1:A:32:THR:HA	1:A:110:PHE:O	2.20	0.41
1:C:145:ILE:HD12	1:C:145:ILE:H	1.86	0.41
1:G:210:LEU:HB3	1:G:211:PRO:HD3	2.02	0.41
1:H:224:TRP:HB2	1:I:281:ILE:HD11	2.02	0.41
1:J:287:GLN:NE2	1:J:290:GLY:O	2.53	0.41
1:A:72:TRP:CD1	1:A:72:TRP:C	2.96	0.41
1:A:140:LEU:HD12	1:A:189:SER:O	2.20	0.41
1:A:234:THR:OG1	1:B:233:GLN:HG2	2.21	0.41
1:B:143:SER:HB3	1:B:168:THR:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:238:LEU:HD12	1:B:238:LEU:HA	1.78	0.41
1:C:174:ARG:HA	1:C:186:ASN:O	2.21	0.41
1:C:212:LEU:HD12	1:C:265:MET:SD	2.61	0.41
1:D:245:TYR:CD2	1:D:266:ILE:HD11	2.56	0.41
1:D:247:LEU:CD2	1:E:247:LEU:HD11	2.50	0.41
1:E:118:LEU:H	1:E:118:LEU:HG	1.44	0.41
1:E:123:ARG:HE	1:E:123:ARG:HB3	1.58	0.41
1:E:145:ILE:HG21	1:E:193:VAL:HG11	2.03	0.41
1:F:287:GLN:NE2	1:F:290:GLY:O	2.54	0.41
1:G:145:ILE:HD13	1:G:166:ALA:HB3	2.02	0.41
1:H:220:TRP:C	1:H:222:VAL:N	2.79	0.41
1:I:143:SER:H	1:I:170:ILE:HD11	1.86	0.41
1:J:208:PHE:HE1	1:J:252:ILE:HG21	1.86	0.41
1:J:256:LEU:HD13	1:J:258:TYR:CE1	2.55	0.41
1:B:130:LEU:HD23	1:B:130:LEU:HA	1.81	0.41
1:B:145:ILE:HD12	1:B:145:ILE:H	1.86	0.41
1:B:212:LEU:HD23	1:B:245:TYR:CD2	2.56	0.41
1:E:72:TRP:CZ3	1:E:135:TYR:CE1	3.09	0.41
1:F:123:ARG:HE	1:F:123:ARG:HB3	1.48	0.41
1:F:174:ARG:HA	1:F:186:ASN:O	2.21	0.41
1:J:72:TRP:CZ3	1:J:135:TYR:CZ	3.09	0.41
1:J:162:ILE:H	1:J:162:ILE:HG12	1.43	0.41
1:A:115:ASP:OD2	1:A:117:ARG:NH2	2.38	0.40
1:D:143:SER:HB3	1:D:168:THR:HG21	2.02	0.40
1:D:205:LEU:HD23	1:D:205:LEU:HA	1.78	0.40
1:F:28:THR:HA	1:F:116:PHE:CE1	2.57	0.40
1:F:140:LEU:HD12	1:F:189:SER:O	2.21	0.40
1:G:118:LEU:H	1:G:118:LEU:HG	1.42	0.40
1:B:255:ARG:O	1:B:256:LEU:HD23	2.21	0.40
1:D:308:PHE:O	1:D:312:GLY:N	2.54	0.40
1:E:67:ILE:HG12	1:E:73:VAL:HG23	2.02	0.40
1:G:95:PHE:HE1	1:G:101:ILE:HD12	1.85	0.40
1:G:238:LEU:HD12	1:G:238:LEU:HA	1.74	0.40
1:H:56:LEU:HD22	1:H:56:LEU:HA	1.69	0.40
1:B:95:PHE:HE1	1:B:101:ILE:HD12	1.86	0.40
1:C:119:PHE:CB	1:C:260:THR:HB	2.50	0.40
1:C:238:LEU:HD12	1:C:238:LEU:HA	1.80	0.40
1:C:252:ILE:HD13	1:C:252:ILE:HA	1.81	0.40
1:D:154:ASN:HD22	1:D:157:ILE:HD12	1.87	0.40
1:F:173:ILE:HD12	1:F:173:ILE:HA	1.86	0.40
1:I:162:ILE:H	1:I:162:ILE:HG12	1.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:178:LEU:HB2	1:I:179:SER:H	1.75	0.40
1:C:173:ILE:HD12	1:C:173:ILE:HA	1.85	0.40
1:E:174:ARG:HA	1:E:186:ASN:O	2.21	0.40
1:F:145:ILE:H	1:F:145:ILE:HD12	1.87	0.40
1:I:67:ILE:HG12	1:I:73:VAL:HG23	2.03	0.40
1:A:278:LEU:HD23	1:A:278:LEU:HA	1.84	0.40
1:B:178:LEU:HB2	1:B:179:SER:H	1.74	0.40
1:C:179:SER:HB3	1:C:180:SER:H	1.68	0.40
1:G:310:ALA:C	1:G:313:CYS:H	2.29	0.40
1:H:145:ILE:HD13	1:H:166:ALA:HB3	2.04	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	305/324 (94%)	252 (83%)	41 (13%)	12 (4%)	2	20
1	B	305/324 (94%)	249 (82%)	40 (13%)	16 (5%)	1	17
1	C	305/324 (94%)	247 (81%)	45 (15%)	13 (4%)	2	19
1	D	305/324 (94%)	254 (83%)	34 (11%)	17 (6%)	1	15
1	E	305/324 (94%)	249 (82%)	39 (13%)	17 (6%)	1	15
1	F	305/324 (94%)	253 (83%)	37 (12%)	15 (5%)	1	17
1	G	305/324 (94%)	250 (82%)	40 (13%)	15 (5%)	1	17
1	H	305/324 (94%)	253 (83%)	33 (11%)	19 (6%)	1	14
1	I	305/324 (94%)	254 (83%)	34 (11%)	17 (6%)	1	15
1	J	305/324 (94%)	247 (81%)	39 (13%)	19 (6%)	1	14
All	All	3050/3240 (94%)	2508 (82%)	382 (12%)	160 (5%)	1	17

All (160) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	119	PHE
1	A	169	HIS
1	A	182	GLN
1	A	202	SER
1	B	119	PHE
1	B	151	ASN
1	B	153	ASP
1	B	169	HIS
1	B	182	GLN
1	B	202	SER
1	C	119	PHE
1	C	169	HIS
1	C	182	GLN
1	C	202	SER
1	D	119	PHE
1	D	169	HIS
1	D	182	GLN
1	D	200	ASN
1	D	202	SER
1	E	119	PHE
1	E	151	ASN
1	E	169	HIS
1	E	182	GLN
1	E	202	SER
1	F	119	PHE
1	F	169	HIS
1	F	182	GLN
1	F	202	SER
1	G	119	PHE
1	G	169	HIS
1	G	182	GLN
1	G	202	SER
1	H	119	PHE
1	H	141	ARG
1	H	148	TYR
1	H	151	ASN
1	H	152	ILE
1	H	169	HIS
1	H	182	GLN
1	H	202	SER
1	H	289	ASN
1	I	119	PHE

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Mol	Chain	Res	Type
1	I	148	TYR
1	I	153	ASP
1	I	169	HIS
1	I	182	GLN
1	I	200	ASN
1	I	202	SER
1	J	119	PHE
1	J	169	HIS
1	J	182	GLN
1	J	200	ASN
1	J	202	SER
1	A	141	ARG
1	A	294	ASP
1	B	141	ARG
1	B	289	ASN
1	B	294	ASP
1	B	295	LEU
1	C	141	ARG
1	C	294	ASP
1	D	294	ASP
1	E	141	ARG
1	E	288	ALA
1	E	294	ASP
1	F	294	ASP
1	F	295	LEU
1	G	141	ARG
1	G	294	ASP
1	H	294	ASP
1	I	141	ARG
1	I	294	ASP
1	J	141	ARG
1	J	149	THR
1	J	294	ASP
1	A	183	PRO
1	A	295	LEU
1	B	200	ASN
1	C	200	ASN
1	C	221	SER
1	C	295	LEU
1	D	141	ARG
1	D	151	ASN
1	D	295	LEU

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Mol	Chain	Res	Type
1	E	200	ASN
1	E	221	SER
1	E	295	LEU
1	F	141	ARG
1	F	200	ASN
1	G	295	LEU
1	H	200	ASN
1	H	221	SER
1	H	295	LEU
1	I	295	LEU
1	J	151	ASN
1	J	221	SER
1	J	288	ALA
1	J	295	LEU
1	A	200	ASN
1	A	221	SER
1	B	184	ASN
1	B	221	SER
1	C	183	PRO
1	C	184	ASN
1	D	183	PRO
1	D	184	ASN
1	E	183	PRO
1	E	184	ASN
1	F	183	PRO
1	F	184	ASN
1	F	221	SER
1	G	88	GLY
1	G	183	PRO
1	G	184	ASN
1	G	221	SER
1	H	183	PRO
1	H	184	ASN
1	I	154	ASN
1	I	183	PRO
1	I	184	ASN
1	J	60	ASN
1	J	183	PRO
1	J	184	ASN
1	B	183	PRO
1	C	25	GLY
1	D	221	SER

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Mol	Chain	Res	Type
1	G	25	GLY
1	G	200	ASN
1	I	221	SER
1	B	257	PRO
1	D	25	GLY
1	D	60	ASN
1	E	257	PRO
1	F	25	GLY
1	H	25	GLY
1	J	25	GLY
1	J	88	GLY
1	A	304	PHE
1	B	304	PHE
1	C	304	PHE
1	D	304	PHE
1	H	304	PHE
1	J	304	PHE
1	D	88	GLY
1	E	304	PHE
1	F	88	GLY
1	F	304	PHE
1	G	257	PRO
1	G	304	PHE
1	I	257	PRO
1	I	304	PHE
1	A	88	GLY
1	I	25	GLY
1	D	257	PRO
1	E	88	GLY
1	H	88	GLY
1	H	257	PRO
1	J	257	PRO
1	E	25	GLY
1	F	257	PRO

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	275/285 (96%)	217 (79%)	58 (21%)	1	6
1	B	275/285 (96%)	217 (79%)	58 (21%)	1	6
1	C	275/285 (96%)	221 (80%)	54 (20%)	1	8
1	D	275/285 (96%)	212 (77%)	63 (23%)	1	5
1	E	275/285 (96%)	218 (79%)	57 (21%)	1	7
1	F	275/285 (96%)	214 (78%)	61 (22%)	1	5
1	G	275/285 (96%)	216 (78%)	59 (22%)	1	6
1	H	275/285 (96%)	216 (78%)	59 (22%)	1	6
1	I	275/285 (96%)	218 (79%)	57 (21%)	1	7
1	J	275/285 (96%)	218 (79%)	57 (21%)	1	7
All	All	2750/2850 (96%)	2167 (79%)	583 (21%)	1	6

All (583) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	VAL
1	A	17	SER
1	A	20	ILE
1	A	22	LYS
1	A	26	VAL
1	A	39	ILE
1	A	43	TRP
1	A	54	LYS
1	A	56	LEU
1	A	63	ILE
1	A	71	LEU
1	A	72	TRP
1	A	73	VAL
1	A	76	LEU
1	A	81	VAL
1	A	87	THR
1	A	91	ARG
1	A	107	LEU
1	A	118	LEU
1	A	123	ARG
1	A	130	LEU
1	A	134	SER
1	A	138	GLN
1	A	145	ILE

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Mol	Chain	Res	Type
1	A	149	THR
1	A	155	GLU
1	A	157	ILE
1	A	162	ILE
1	A	165	LYS
1	A	168	THR
1	A	179	SER
1	A	182	GLN
1	A	207	SER
1	A	208	PHE
1	A	209	ILE
1	A	219	SER
1	A	232	LEU
1	A	234	THR
1	A	237	THR
1	A	238	LEU
1	A	247	LEU
1	A	252	ILE
1	A	253	LEU
1	A	255	ARG
1	A	259	THR
1	A	261	VAL
1	A	262	ILE
1	A	265	MET
1	A	266	ILE
1	A	277	ILE
1	A	279	LEU
1	A	281	ILE
1	A	287	GLN
1	A	291	VAL
1	A	296	LEU
1	A	304	PHE
1	A	313	CYS
1	A	314	VAL
1	B	12	VAL
1	B	20	ILE
1	B	22	LYS
1	B	26	VAL
1	B	39	ILE
1	B	54	LYS
1	B	56	LEU
1	B	63	ILE

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Mol	Chain	Res	Type
1	B	71	LEU
1	B	72	TRP
1	B	73	VAL
1	B	76	LEU
1	B	81	VAL
1	B	87	THR
1	B	91	ARG
1	B	107	LEU
1	B	118	LEU
1	B	123	ARG
1	B	130	LEU
1	B	134	SER
1	B	138	GLN
1	B	145	ILE
1	B	150	GLU
1	B	152	ILE
1	B	155	GLU
1	B	157	ILE
1	B	162	ILE
1	B	165	LYS
1	B	168	THR
1	B	178	LEU
1	B	179	SER
1	B	182	GLN
1	B	207	SER
1	B	208	PHE
1	B	212	LEU
1	B	219	SER
1	B	229	SER
1	B	232	LEU
1	B	234	THR
1	B	237	THR
1	B	238	LEU
1	B	247	LEU
1	B	252	ILE
1	B	253	LEU
1	B	255	ARG
1	B	259	THR
1	B	261	VAL
1	B	262	ILE
1	B	265	MET
1	B	266	ILE

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Mol	Chain	Res	Type
1	B	277	ILE
1	B	279	LEU
1	B	281	ILE
1	B	287	GLN
1	B	291	VAL
1	B	296	LEU
1	B	304	PHE
1	B	316	VAL
1	C	12	VAL
1	C	17	SER
1	C	20	ILE
1	C	22	LYS
1	C	26	VAL
1	C	39	ILE
1	C	54	LYS
1	C	56	LEU
1	C	63	ILE
1	C	71	LEU
1	C	72	TRP
1	C	73	VAL
1	C	76	LEU
1	C	81	VAL
1	C	87	THR
1	C	91	ARG
1	C	107	LEU
1	C	118	LEU
1	C	123	ARG
1	C	130	LEU
1	C	134	SER
1	C	138	GLN
1	C	145	ILE
1	C	146	GLN
1	C	155	GLU
1	C	157	ILE
1	C	162	ILE
1	C	168	THR
1	C	179	SER
1	C	182	GLN
1	C	207	SER
1	C	208	PHE
1	C	212	LEU
1	C	219	SER

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Mol	Chain	Res	Type
1	C	232	LEU
1	C	234	THR
1	C	237	THR
1	C	238	LEU
1	C	247	LEU
1	C	252	ILE
1	C	253	LEU
1	C	255	ARG
1	C	259	THR
1	C	261	VAL
1	C	262	ILE
1	C	265	MET
1	C	266	ILE
1	C	277	ILE
1	C	279	LEU
1	C	281	ILE
1	C	287	GLN
1	C	291	VAL
1	C	296	LEU
1	C	304	PHE
1	D	12	VAL
1	D	17	SER
1	D	20	ILE
1	D	22	LYS
1	D	26	VAL
1	D	35	VAL
1	D	39	ILE
1	D	43	TRP
1	D	54	LYS
1	D	56	LEU
1	D	63	ILE
1	D	71	LEU
1	D	72	TRP
1	D	73	VAL
1	D	76	LEU
1	D	81	VAL
1	D	87	THR
1	D	91	ARG
1	D	107	LEU
1	D	118	LEU
1	D	123	ARG
1	D	130	LEU

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Mol	Chain	Res	Type
1	D	134	SER
1	D	138	GLN
1	D	145	ILE
1	D	150	GLU
1	D	151	ASN
1	D	155	GLU
1	D	157	ILE
1	D	162	ILE
1	D	165	LYS
1	D	168	THR
1	D	178	LEU
1	D	179	SER
1	D	182	GLN
1	D	207	SER
1	D	208	PHE
1	D	212	LEU
1	D	219	SER
1	D	232	LEU
1	D	234	THR
1	D	237	THR
1	D	238	LEU
1	D	247	LEU
1	D	252	ILE
1	D	253	LEU
1	D	255	ARG
1	D	259	THR
1	D	261	VAL
1	D	262	ILE
1	D	265	MET
1	D	266	ILE
1	D	277	ILE
1	D	279	LEU
1	D	281	ILE
1	D	287	GLN
1	D	289	ASN
1	D	291	VAL
1	D	296	LEU
1	D	304	PHE
1	D	314	VAL
1	D	316	VAL
1	D	317	ILE
1	E	12	VAL

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Mol	Chain	Res	Type
1	E	20	ILE
1	E	22	LYS
1	E	26	VAL
1	E	39	ILE
1	E	43	TRP
1	E	54	LYS
1	E	56	LEU
1	E	63	ILE
1	E	71	LEU
1	E	72	TRP
1	E	73	VAL
1	E	76	LEU
1	E	81	VAL
1	E	87	THR
1	E	91	ARG
1	E	107	LEU
1	E	118	LEU
1	E	123	ARG
1	E	130	LEU
1	E	134	SER
1	E	138	GLN
1	E	145	ILE
1	E	149	THR
1	E	153	ASP
1	E	155	GLU
1	E	157	ILE
1	E	162	ILE
1	E	168	THR
1	E	179	SER
1	E	182	GLN
1	E	185	GLN
1	E	207	SER
1	E	208	PHE
1	E	212	LEU
1	E	219	SER
1	E	232	LEU
1	E	234	THR
1	E	237	THR
1	E	238	LEU
1	E	247	LEU
1	E	252	ILE
1	E	255	ARG

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Mol	Chain	Res	Type
1	E	259	THR
1	E	261	VAL
1	E	262	ILE
1	E	265	MET
1	E	266	ILE
1	E	277	ILE
1	E	279	LEU
1	E	281	ILE
1	E	287	GLN
1	E	291	VAL
1	E	296	LEU
1	E	304	PHE
1	E	314	VAL
1	E	315	LEU
1	F	12	VAL
1	F	17	SER
1	F	20	ILE
1	F	22	LYS
1	F	26	VAL
1	F	39	ILE
1	F	54	LYS
1	F	56	LEU
1	F	63	ILE
1	F	71	LEU
1	F	72	TRP
1	F	73	VAL
1	F	76	LEU
1	F	81	VAL
1	F	87	THR
1	F	91	ARG
1	F	107	LEU
1	F	118	LEU
1	F	123	ARG
1	F	130	LEU
1	F	134	SER
1	F	138	GLN
1	F	145	ILE
1	F	149	THR
1	F	150	GLU
1	F	152	ILE
1	F	153	ASP
1	F	155	GLU

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Mol	Chain	Res	Type
1	F	157	ILE
1	F	162	ILE
1	F	165	LYS
1	F	168	THR
1	F	173	ILE
1	F	179	SER
1	F	182	GLN
1	F	207	SER
1	F	208	PHE
1	F	212	LEU
1	F	219	SER
1	F	232	LEU
1	F	234	THR
1	F	237	THR
1	F	238	LEU
1	F	247	LEU
1	F	252	ILE
1	F	253	LEU
1	F	255	ARG
1	F	259	THR
1	F	261	VAL
1	F	262	ILE
1	F	265	MET
1	F	266	ILE
1	F	277	ILE
1	F	279	LEU
1	F	281	ILE
1	F	287	GLN
1	F	291	VAL
1	F	296	LEU
1	F	304	PHE
1	F	311	ILE
1	F	317	ILE
1	G	12	VAL
1	G	20	ILE
1	G	22	LYS
1	G	26	VAL
1	G	39	ILE
1	G	43	TRP
1	G	54	LYS
1	G	56	LEU
1	G	63	ILE

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Mol	Chain	Res	Type
1	G	71	LEU
1	G	72	TRP
1	G	73	VAL
1	G	76	LEU
1	G	81	VAL
1	G	87	THR
1	G	90	LYS
1	G	91	ARG
1	G	107	LEU
1	G	118	LEU
1	G	123	ARG
1	G	130	LEU
1	G	134	SER
1	G	138	GLN
1	G	145	ILE
1	G	149	THR
1	G	151	ASN
1	G	152	ILE
1	G	155	GLU
1	G	157	ILE
1	G	162	ILE
1	G	168	THR
1	G	179	SER
1	G	182	GLN
1	G	207	SER
1	G	208	PHE
1	G	212	LEU
1	G	219	SER
1	G	232	LEU
1	G	234	THR
1	G	237	THR
1	G	238	LEU
1	G	247	LEU
1	G	252	ILE
1	G	253	LEU
1	G	255	ARG
1	G	259	THR
1	G	261	VAL
1	G	262	ILE
1	G	265	MET
1	G	266	ILE
1	G	277	ILE

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Mol	Chain	Res	Type
1	G	279	LEU
1	G	281	ILE
1	G	287	GLN
1	G	291	VAL
1	G	296	LEU
1	G	304	PHE
1	G	313	CYS
1	G	317	ILE
1	H	12	VAL
1	H	17	SER
1	H	20	ILE
1	H	22	LYS
1	H	26	VAL
1	H	35	VAL
1	H	39	ILE
1	H	54	LYS
1	H	56	LEU
1	H	63	ILE
1	H	71	LEU
1	H	72	TRP
1	H	73	VAL
1	H	76	LEU
1	H	81	VAL
1	H	87	THR
1	H	91	ARG
1	H	107	LEU
1	H	118	LEU
1	H	123	ARG
1	H	130	LEU
1	H	134	SER
1	H	138	GLN
1	H	145	ILE
1	H	146	GLN
1	H	149	THR
1	H	155	GLU
1	H	157	ILE
1	H	162	ILE
1	H	165	LYS
1	H	168	THR
1	H	178	LEU
1	H	182	GLN
1	H	207	SER

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Mol	Chain	Res	Type
1	H	208	PHE
1	H	212	LEU
1	H	219	SER
1	H	232	LEU
1	H	234	THR
1	H	237	THR
1	H	238	LEU
1	H	247	LEU
1	H	252	ILE
1	H	253	LEU
1	H	255	ARG
1	H	259	THR
1	H	261	VAL
1	H	262	ILE
1	H	265	MET
1	H	266	ILE
1	H	277	ILE
1	H	279	LEU
1	H	281	ILE
1	H	287	GLN
1	H	291	VAL
1	H	296	LEU
1	H	304	PHE
1	H	316	VAL
1	H	317	ILE
1	I	12	VAL
1	I	17	SER
1	I	20	ILE
1	I	22	LYS
1	I	26	VAL
1	I	39	ILE
1	I	54	LYS
1	I	56	LEU
1	I	63	ILE
1	I	71	LEU
1	I	72	TRP
1	I	73	VAL
1	I	76	LEU
1	I	81	VAL
1	I	87	THR
1	I	91	ARG
1	I	93	MET

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Mol	Chain	Res	Type
1	I	107	LEU
1	I	118	LEU
1	I	123	ARG
1	I	130	LEU
1	I	134	SER
1	I	138	GLN
1	I	145	ILE
1	I	146	GLN
1	I	152	ILE
1	I	154	ASN
1	I	157	ILE
1	I	162	ILE
1	I	168	THR
1	I	182	GLN
1	I	185	GLN
1	I	207	SER
1	I	208	PHE
1	I	212	LEU
1	I	219	SER
1	I	232	LEU
1	I	234	THR
1	I	237	THR
1	I	238	LEU
1	I	247	LEU
1	I	252	ILE
1	I	253	LEU
1	I	255	ARG
1	I	259	THR
1	I	261	VAL
1	I	262	ILE
1	I	265	MET
1	I	266	ILE
1	I	277	ILE
1	I	279	LEU
1	I	281	ILE
1	I	287	GLN
1	I	289	ASN
1	I	291	VAL
1	I	296	LEU
1	I	304	PHE
1	J	12	VAL
1	J	17	SER

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Mol	Chain	Res	Type
1	J	20	ILE
1	J	22	LYS
1	J	26	VAL
1	J	39	ILE
1	J	43	TRP
1	J	54	LYS
1	J	56	LEU
1	J	63	ILE
1	J	71	LEU
1	J	72	TRP
1	J	73	VAL
1	J	76	LEU
1	J	81	VAL
1	J	87	THR
1	J	90	LYS
1	J	91	ARG
1	J	107	LEU
1	J	118	LEU
1	J	123	ARG
1	J	130	LEU
1	J	134	SER
1	J	138	GLN
1	J	145	ILE
1	J	149	THR
1	J	155	GLU
1	J	157	ILE
1	J	162	ILE
1	J	165	LYS
1	J	168	THR
1	J	182	GLN
1	J	207	SER
1	J	208	PHE
1	J	212	LEU
1	J	219	SER
1	J	232	LEU
1	J	234	THR
1	J	237	THR
1	J	238	LEU
1	J	247	LEU
1	J	252	ILE
1	J	253	LEU
1	J	255	ARG

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Mol	Chain	Res	Type
1	J	259	THR
1	J	261	VAL
1	J	262	ILE
1	J	265	MET
1	J	266	ILE
1	J	277	ILE
1	J	279	LEU
1	J	281	ILE
1	J	287	GLN
1	J	291	VAL
1	J	296	LEU
1	J	304	PHE
1	J	311	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	GLN
1	A	124	GLN
1	A	233	GLN
1	A	285	HIS
1	A	289	ASN
1	B	124	GLN
1	B	233	GLN
1	B	285	HIS
1	C	62	GLN
1	C	124	GLN
1	C	285	HIS
1	D	124	GLN
1	D	233	GLN
1	E	62	GLN
1	E	124	GLN
1	E	233	GLN
1	E	285	HIS
1	F	62	GLN
1	F	124	GLN
1	F	233	GLN
1	F	285	HIS
1	F	289	ASN
1	G	124	GLN
1	G	151	ASN
1	G	233	GLN

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Mol	Chain	Res	Type
1	G	285	HIS
1	G	287	GLN
1	G	289	ASN
1	H	62	GLN
1	H	124	GLN
1	H	233	GLN
1	H	284	HIS
1	H	287	GLN
1	I	124	GLN
1	I	151	ASN
1	I	154	ASN
1	I	233	GLN
1	I	285	HIS
1	I	287	GLN
1	J	124	GLN
1	J	233	GLN
1	J	285	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

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	307/324 (94%)	-0.44	1 (0%) 90 78	79, 119, 201, 239	0
1	B	307/324 (94%)	-0.28	2 (0%) 84 65	80, 117, 208, 254	0
1	C	307/324 (94%)	-0.37	0 100 100	77, 118, 206, 237	0
1	D	307/324 (94%)	-0.28	1 (0%) 90 78	77, 116, 200, 260	0
1	E	307/324 (94%)	-0.29	1 (0%) 90 78	78, 119, 212, 260	0
1	F	307/324 (94%)	-0.40	3 (0%) 79 58	78, 119, 199, 236	0
1	G	307/324 (94%)	-0.34	3 (0%) 79 58	76, 116, 195, 238	0
1	H	307/324 (94%)	-0.37	0 100 100	80, 118, 208, 239	0
1	I	307/324 (94%)	-0.26	4 (1%) 75 53	78, 118, 206, 255	0
1	J	307/324 (94%)	-0.34	1 (0%) 90 78	77, 119, 199, 238	0
All	All	3070/3240 (94%)	-0.34	16 (0%) 87 71	76, 118, 207, 260	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	292	GLU	4.1
1	I	157	ILE	3.7
1	B	291	VAL	3.0
1	G	289	ASN	2.9
1	I	181	VAL	2.5
1	I	152	ILE	2.4
1	A	179	SER	2.3
1	D	179	SER	2.3
1	E	305	PRO	2.3
1	B	152	ILE	2.2
1	F	290	GLY	2.2
1	G	179	SER	2.1
1	G	83	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	J	179	SER	2.0
1	F	181	VAL	2.0
1	I	291	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 oligosaccharides 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.