



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 08:45 PM EDT

PDB ID : 5HEU
Title : Pentameric ligand-gated ion channel ELIC mutant A257Y
Authors : Bertozzi, C.; Dutzler, R.
Deposited on : 2016-01-06
Resolution : 3.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

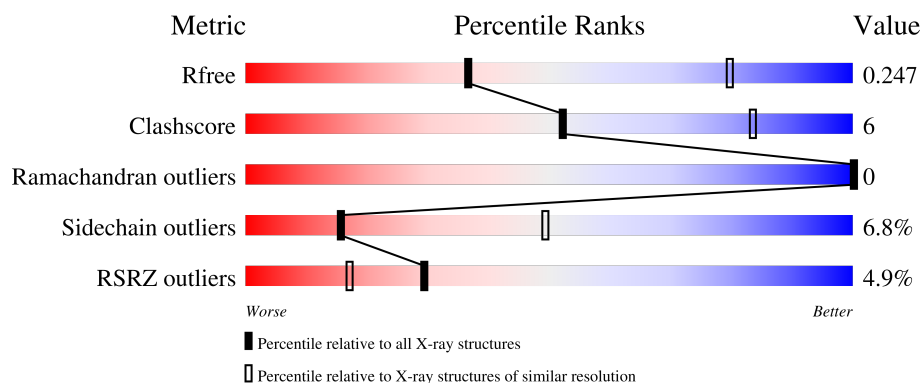
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	322	<div> <div>4%</div> <div>78% 17% • 5%</div> </div>
1	B	322	<div> <div>4%</div> <div>76% 17% • 5%</div> </div>
1	C	322	<div> <div>6%</div> <div>76% 18% • 5%</div> </div>
1	D	322	<div> <div>3%</div> <div>80% 13% • 5%</div> </div>
1	E	322	<div> <div>3%</div> <div>76% 18% • 5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	322	<div><div></div><div>76%18%5%</div><div>7%<div></div></div></div>
1	G	322	<div><div></div><div>76%18%5%</div><div>4%<div></div></div></div>
1	H	322	<div><div></div><div>77%17%5%</div><div>7%<div></div></div></div>
1	I	322	<div><div></div><div>78%15%5%</div><div>5%<div></div></div></div>
1	J	322	<div><div></div><div>75%20%5%</div><div>4%<div></div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 24980 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
			2498	1627	416	449	6			
1	B	307	Total	C	N	O	S	0	0	0
			2498	1627	416	449	6			
1	C	307	Total	C	N	O	S	0	0	0
			2498	1627	416	449	6			
1	D	307	Total	C	N	O	S	0	0	0
			2498	1627	416	449	6			
1	E	307	Total	C	N	O	S	0	0	0
			2498	1627	416	449	6			
1	F	307	Total	C	N	O	S	0	0	0
			2498	1627	416	449	6			
1	G	307	Total	C	N	O	S	0	0	0
			2498	1627	416	449	6			
1	H	307	Total	C	N	O	S	0	0	0
			2498	1627	416	449	6			
1	I	307	Total	C	N	O	S	0	0	0
			2498	1627	416	449	6			
1	J	307	Total	C	N	O	S	0	0	0
			2498	1627	416	449	6			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	258	ALA	TYR	engineered mutation	UNP E0SJQ4
B	258	ALA	TYR	engineered mutation	UNP E0SJQ4
C	258	ALA	TYR	engineered mutation	UNP E0SJQ4
D	258	ALA	TYR	engineered mutation	UNP E0SJQ4
E	258	ALA	TYR	engineered mutation	UNP E0SJQ4
F	258	ALA	TYR	engineered mutation	UNP E0SJQ4
G	258	ALA	TYR	engineered mutation	UNP E0SJQ4
H	258	ALA	TYR	engineered mutation	UNP E0SJQ4
I	258	ALA	TYR	engineered mutation	UNP E0SJQ4

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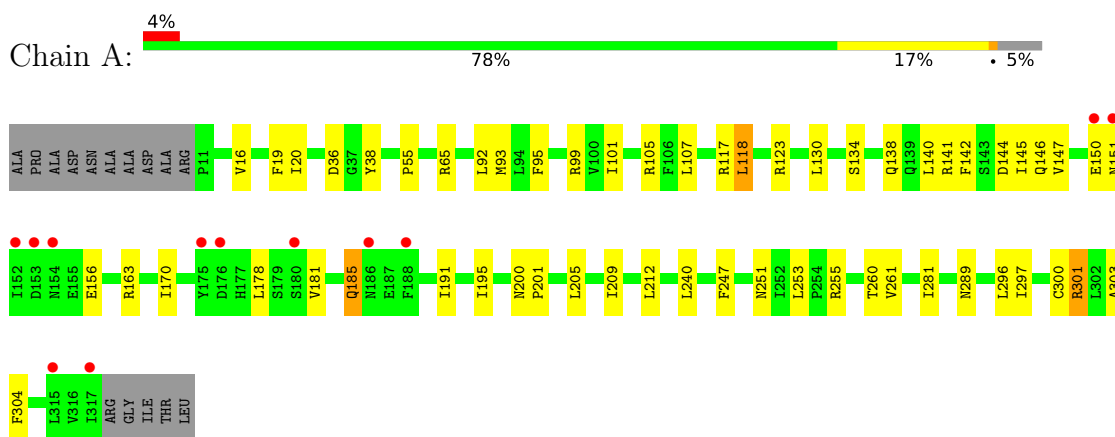
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Chain	Residue	Modelled	Actual	Comment	Reference
J	258	ALA	TYR	engineered mutation	UNP E0SJQ4

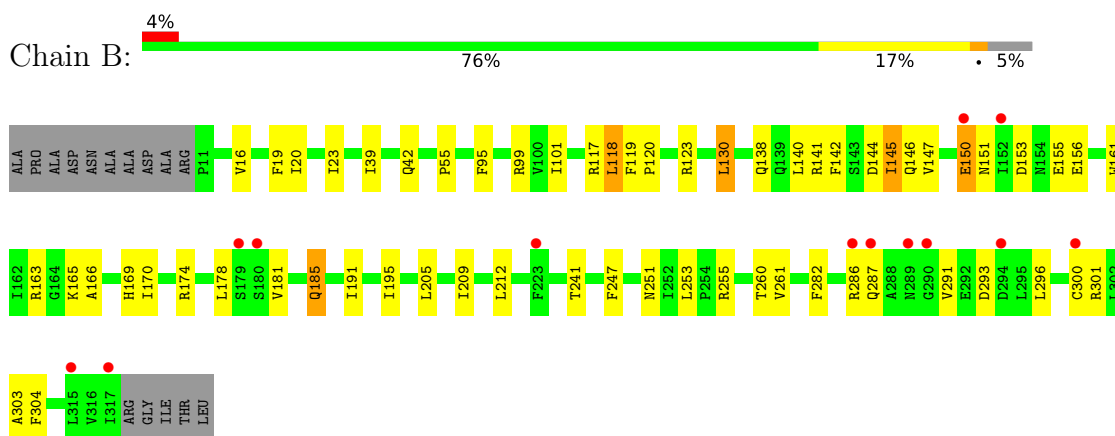
3 Residue-property plots [i](#)

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.

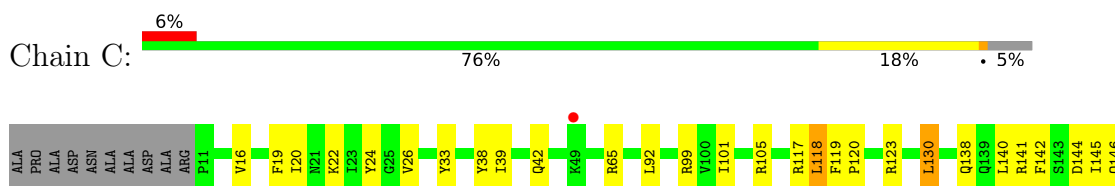
- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

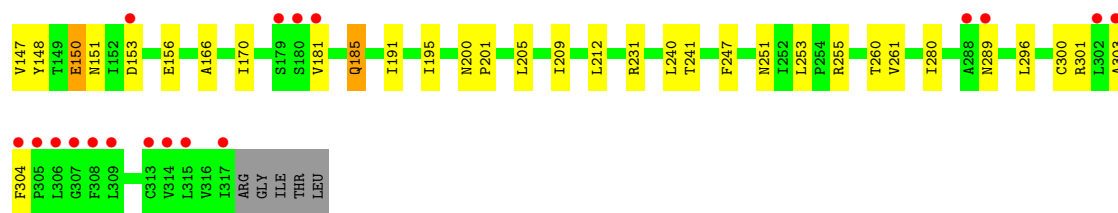


- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

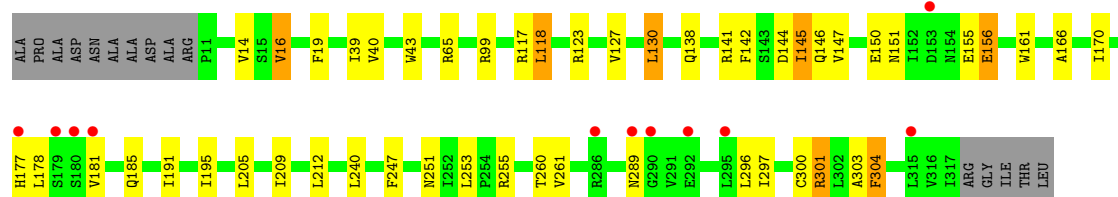
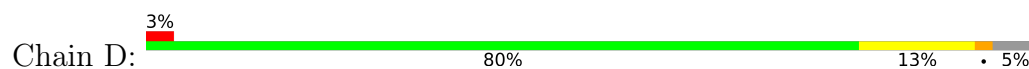


- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

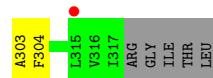
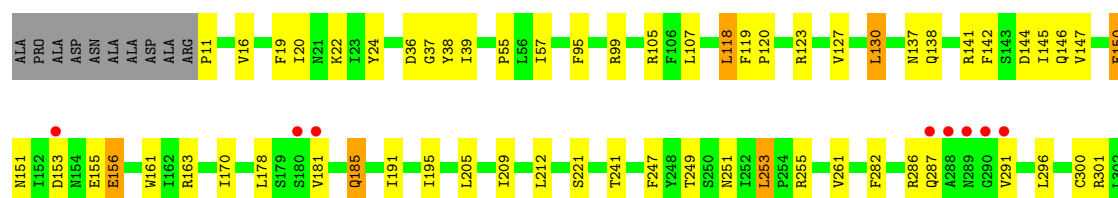
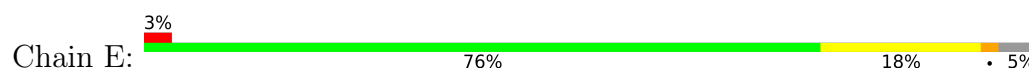




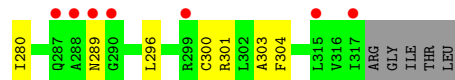
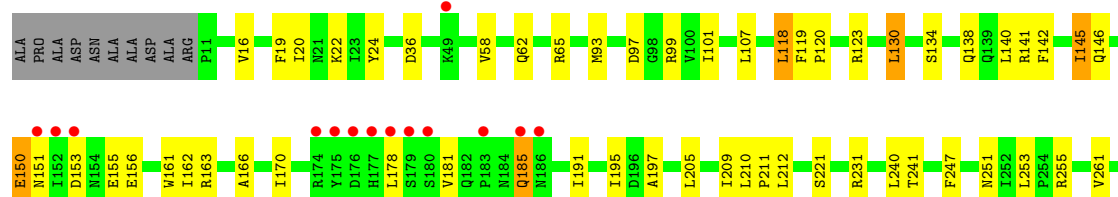
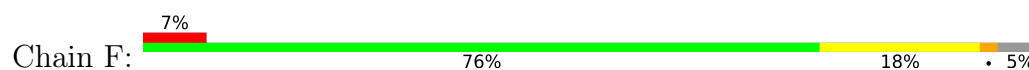
• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



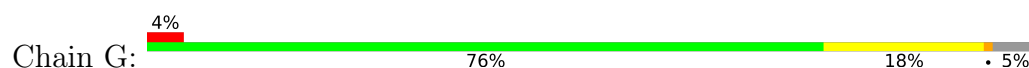
• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

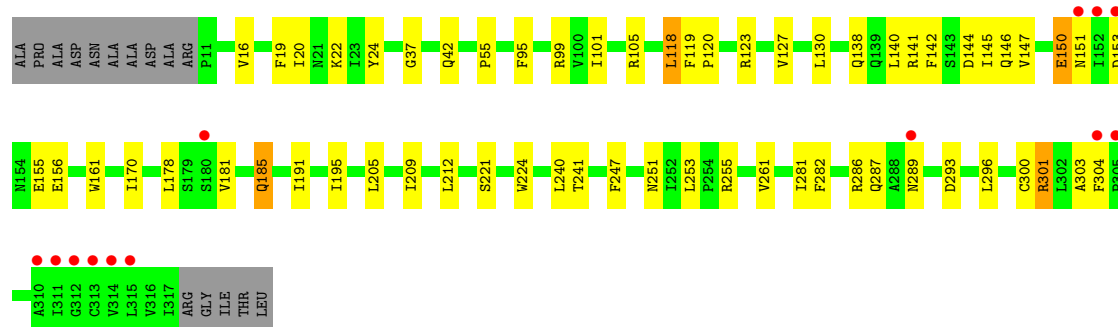


• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

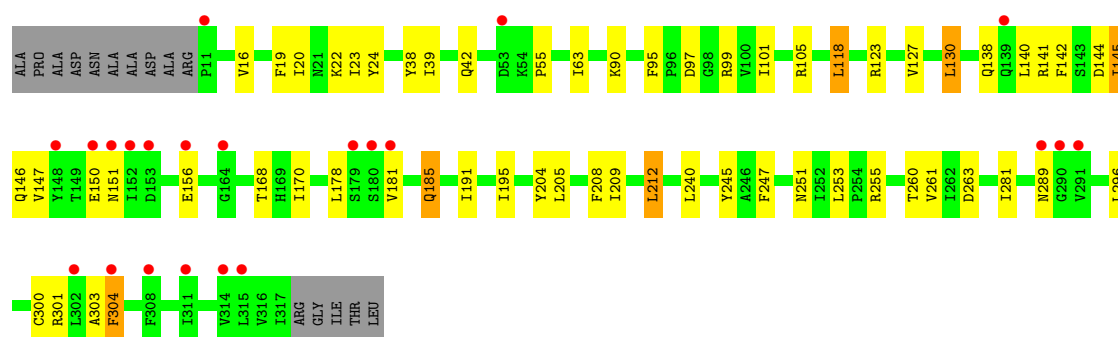
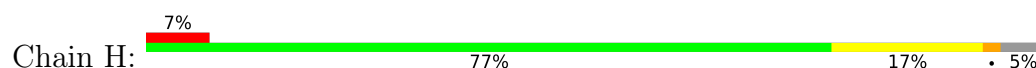


• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

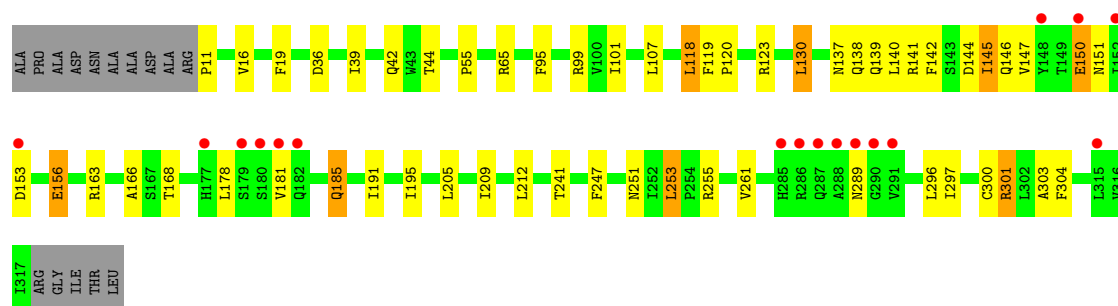
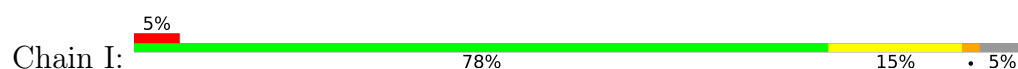




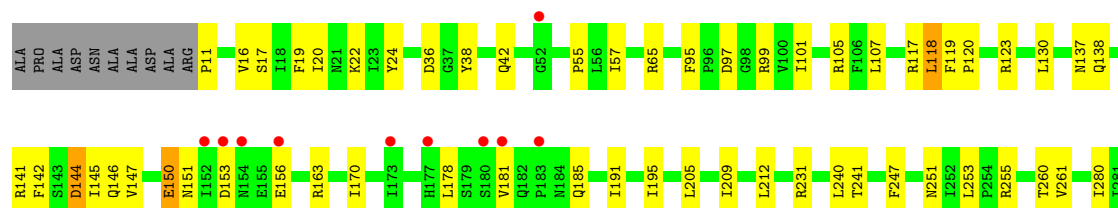
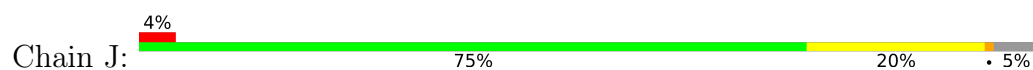
- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

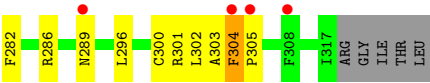


- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



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





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.00Å 266.61Å 110.71Å 90.00° 110.47° 90.00°	Depositor
Resolution (Å)	29.94 – 3.20 49.18 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.94-3.20) 99.5 (49.18-3.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.220 , 0.247 0.221 , 0.247	Depositor DCC
R_{free} test set	4694 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	83.0	Xtriage
Anisotropy	0.467	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	24980	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.25	0/2565	0.43	0/3496
1	B	0.26	0/2565	0.43	0/3496
1	C	0.25	0/2565	0.43	0/3496
1	D	0.26	0/2565	0.43	0/3496
1	E	0.25	0/2565	0.43	0/3496
1	F	0.25	0/2565	0.43	0/3496
1	G	0.26	0/2565	0.43	0/3496
1	H	0.25	0/2565	0.43	0/3496
1	I	0.25	0/2565	0.43	0/3496
1	J	0.25	0/2565	0.43	0/3496
All	All	0.25	0/25650	0.43	0/34960

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2498	0	2474	27	0
1	B	2498	0	2474	34	0
1	C	2498	0	2474	29	0
1	D	2498	0	2474	24	0
1	E	2498	0	2474	34	0
1	F	2498	0	2474	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	2498	0	2474	28	0
1	H	2498	0	2474	30	0
1	I	2498	0	2474	32	0
1	J	2498	0	2474	31	0
All	All	24980	0	24740	274	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 6.

All (274) 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:F:300:CYS:HA	1:F:303:ALA:HB3	1.76	0.68
1:H:251:ASN:O	1:H:255:ARG:NH1	2.28	0.67
1:B:170:ILE:HG12	1:B:191:ILE:HG12	1.77	0.66
1:A:300:CYS:HA	1:A:303:ALA:HB3	1.77	0.66
1:D:300:CYS:HA	1:D:303:ALA:HB3	1.79	0.64
1:A:170:ILE:HG12	1:A:191:ILE:HG12	1.80	0.63
1:H:300:CYS:HA	1:H:303:ALA:HB3	1.79	0.62
1:I:251:ASN:O	1:I:255:ARG:NH1	2.33	0.62
1:I:300:CYS:HA	1:I:303:ALA:HB3	1.80	0.62
1:I:205:LEU:HD23	1:I:209:ILE:HD12	1.82	0.62
1:B:300:CYS:HA	1:B:303:ALA:HB3	1.81	0.62
1:E:300:CYS:HA	1:E:303:ALA:HB3	1.81	0.61
1:E:251:ASN:O	1:E:255:ARG:NH1	2.34	0.61
1:D:205:LEU:HD23	1:D:209:ILE:HD12	1.83	0.61
1:A:205:LEU:HD23	1:A:209:ILE:HD12	1.82	0.61
1:B:174:ARG:NH2	1:I:139:GLN:OE1	2.34	0.61
1:G:251:ASN:O	1:G:255:ARG:NH1	2.33	0.61
1:J:300:CYS:HA	1:J:303:ALA:HB3	1.83	0.60
1:C:300:CYS:HA	1:C:303:ALA:HB3	1.82	0.60
1:B:205:LEU:HD23	1:B:209:ILE:HD12	1.85	0.59
1:B:118:LEU:HA	1:B:261:VAL:HG23	1.83	0.58
1:F:170:ILE:HG12	1:F:191:ILE:HG12	1.84	0.58
1:B:251:ASN:O	1:B:255:ARG:NH1	2.36	0.58
1:F:251:ASN:O	1:F:255:ARG:NH1	2.36	0.58
1:G:300:CYS:HA	1:G:303:ALA:HB3	1.84	0.58
1:D:118:LEU:HA	1:D:261:VAL:HG23	1.85	0.58
1:A:251:ASN:O	1:A:255:ARG:NH1	2.37	0.57
1:J:251:ASN:O	1:J:255:ARG:NH1	2.37	0.57
1:D:251:ASN:O	1:D:255:ARG:NH1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:205:LEU:HD23	1:J:209:ILE:HD12	1.87	0.57
1:I:118:LEU:HA	1:I:261:VAL:HG23	1.87	0.57
1:H:118:LEU:HA	1:H:261:VAL:HG23	1.87	0.57
1:F:118:LEU:HA	1:F:261:VAL:HG23	1.86	0.56
1:G:205:LEU:HD23	1:G:209:ILE:HD12	1.87	0.56
1:H:170:ILE:HG12	1:H:191:ILE:HG12	1.87	0.56
1:C:118:LEU:HA	1:C:261:VAL:HG23	1.86	0.56
1:C:251:ASN:O	1:C:255:ARG:NH1	2.39	0.56
1:F:205:LEU:HD23	1:F:209:ILE:HD12	1.88	0.56
1:F:240:LEU:HD13	1:J:241:THR:HA	1.88	0.56
1:B:166:ALA:HB2	1:B:195:ILE:HG12	1.87	0.55
1:D:118:LEU:H	1:D:118:LEU:HD12	1.72	0.55
1:H:205:LEU:HD23	1:H:209:ILE:HD12	1.89	0.55
1:E:118:LEU:HA	1:E:261:VAL:HG23	1.90	0.54
1:E:36:ASP:HB2	1:E:107:LEU:HD13	1.90	0.54
1:D:170:ILE:HG12	1:D:191:ILE:HG12	1.90	0.54
1:E:249:THR:HG23	1:E:253:LEU:HD23	1.90	0.54
1:C:170:ILE:HG12	1:C:191:ILE:HG12	1.89	0.54
1:C:205:LEU:HD23	1:C:209:ILE:HD12	1.90	0.53
1:J:118:LEU:HA	1:J:261:VAL:HG23	1.90	0.53
1:D:166:ALA:HB2	1:D:195:ILE:HG12	1.90	0.53
1:C:39:ILE:HD11	1:C:130:LEU:HD11	1.91	0.53
1:E:155:GLU:O	1:E:161:TRP:NE1	2.39	0.53
1:E:170:ILE:HG12	1:E:191:ILE:HG12	1.89	0.53
1:I:19:PHE:CE2	1:I:146:GLN:HG3	2.44	0.53
1:A:118:LEU:HA	1:A:261:VAL:HG23	1.91	0.52
1:F:181:VAL:HG21	1:J:99:ARG:NH2	2.24	0.52
1:I:39:ILE:HD11	1:I:130:LEU:HD11	1.92	0.51
1:D:99:ARG:NH2	1:E:181:VAL:HG21	2.26	0.51
1:E:19:PHE:CE2	1:E:146:GLN:HG3	2.46	0.51
1:J:170:ILE:HG12	1:J:191:ILE:HG12	1.93	0.51
1:D:147:VAL:HG21	1:D:195:ILE:HD13	1.92	0.51
1:H:39:ILE:HD11	1:H:130:LEU:HD11	1.92	0.51
1:E:150:GLU:HG3	1:E:153:ASP:HB3	1.92	0.51
1:G:99:ARG:NH2	1:H:181:VAL:HG21	2.26	0.51
1:G:170:ILE:HG12	1:G:191:ILE:HG12	1.94	0.50
1:D:156:GLU:CD	1:D:156:GLU:H	2.15	0.50
1:G:287:GLN:HG3	1:G:293:ASP:HB2	1.92	0.50
1:H:22:LYS:HE3	1:H:24:TYR:CD1	2.47	0.50
1:B:19:PHE:CE2	1:B:146:GLN:HG3	2.47	0.50
1:D:19:PHE:CE2	1:D:146:GLN:HG3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:155:GLU:O	1:G:161:TRP:NE1	2.43	0.50
1:A:20:ILE:HD12	1:A:195:ILE:HD11	1.94	0.49
1:A:147:VAL:HG21	1:A:195:ILE:HD13	1.93	0.49
1:D:39:ILE:HD11	1:D:130:LEU:HD11	1.95	0.49
1:F:22:LYS:HE3	1:F:24:TYR:CD1	2.47	0.49
1:J:141:ARG:HG3	1:J:142:PHE:CD2	2.47	0.49
1:A:141:ARG:HG3	1:A:142:PHE:CD2	2.48	0.49
1:F:118:LEU:HD12	1:F:118:LEU:H	1.77	0.49
1:B:39:ILE:HD11	1:B:130:LEU:HD11	1.94	0.49
1:B:140:LEU:HD13	1:B:191:ILE:HG13	1.93	0.49
1:B:141:ARG:HG3	1:B:142:PHE:CD2	2.47	0.49
1:H:20:ILE:HD12	1:H:195:ILE:HD11	1.93	0.49
1:C:118:LEU:HD12	1:C:118:LEU:H	1.78	0.49
1:H:99:ARG:NH2	1:I:181:VAL:HG21	2.28	0.49
1:C:231:ARG:HB3	1:C:280:ILE:HD13	1.95	0.49
1:H:141:ARG:HG3	1:H:142:PHE:CD2	2.48	0.48
1:I:141:ARG:HG3	1:I:142:PHE:CD2	2.48	0.48
1:I:156:GLU:CD	1:I:156:GLU:H	2.16	0.48
1:F:140:LEU:HD13	1:F:191:ILE:HG13	1.95	0.48
1:F:141:ARG:HG3	1:F:142:PHE:CD2	2.47	0.48
1:I:36:ASP:HB2	1:I:107:LEU:HD13	1.94	0.48
1:G:118:LEU:HA	1:G:261:VAL:HG23	1.94	0.48
1:G:141:ARG:HG3	1:G:142:PHE:CD2	2.48	0.48
1:F:19:PHE:CE2	1:F:146:GLN:HG3	2.49	0.48
1:J:36:ASP:HB2	1:J:107:LEU:HD13	1.95	0.48
1:B:241:THR:HA	1:C:240:LEU:HD13	1.96	0.48
1:H:19:PHE:CE2	1:H:146:GLN:HG3	2.49	0.48
1:D:141:ARG:HG3	1:D:142:PHE:CD2	2.49	0.47
1:B:282:PHE:CZ	1:B:286:ARG:HG3	2.50	0.47
1:E:55:PRO:HB3	1:E:95:PHE:CD1	2.50	0.47
1:A:36:ASP:HB2	1:A:107:LEU:HD13	1.95	0.47
1:C:141:ARG:HG3	1:C:142:PHE:CD2	2.49	0.47
1:B:150:GLU:HG3	1:B:153:ASP:HB3	1.96	0.47
1:E:141:ARG:HG3	1:E:142:PHE:CD2	2.49	0.47
1:G:150:GLU:HG3	1:G:153:ASP:HB3	1.96	0.47
1:J:150:GLU:HG3	1:J:153:ASP:HB3	1.95	0.47
1:B:117:ARG:O	1:B:260:THR:HA	2.14	0.47
1:B:147:VAL:HG21	1:B:195:ILE:HD13	1.97	0.46
1:G:241:THR:HA	1:H:240:LEU:HD13	1.97	0.46
1:I:42:GLN:HG3	1:I:101:ILE:HG12	1.96	0.46
1:B:20:ILE:HD12	1:B:195:ILE:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:147:VAL:HG21	1:H:195:ILE:HD13	1.96	0.46
1:J:22:LYS:HE3	1:J:24:TYR:CD1	2.51	0.46
1:F:150:GLU:HG3	1:F:153:ASP:HB3	1.97	0.46
1:A:281:ILE:HD11	1:E:221:SER:HB2	1.98	0.46
1:A:163:ARG:HD3	1:A:163:ARG:HA	1.72	0.46
1:C:19:PHE:CE2	1:C:146:GLN:HG3	2.51	0.46
1:I:118:LEU:HD12	1:I:118:LEU:H	1.81	0.46
1:C:42:GLN:HG3	1:C:101:ILE:HG12	1.98	0.46
1:B:118:LEU:HD12	1:B:118:LEU:H	1.81	0.45
1:B:23:ILE:HD11	1:B:195:ILE:HD12	1.99	0.45
1:B:145:ILE:HG13	1:B:166:ALA:HB3	1.99	0.45
1:C:99:ARG:NH2	1:D:181:VAL:HG21	2.31	0.45
1:E:39:ILE:HD11	1:E:130:LEU:HD11	1.97	0.45
1:J:42:GLN:HG3	1:J:101:ILE:HG12	1.98	0.45
1:B:99:ARG:NH2	1:C:181:VAL:HG21	2.32	0.45
1:G:19:PHE:CE2	1:G:146:GLN:HG3	2.51	0.45
1:J:38:TYR:CZ	1:J:105:ARG:HD3	2.51	0.45
1:F:145:ILE:HG13	1:F:166:ALA:HB3	1.98	0.45
1:F:163:ARG:HD3	1:F:163:ARG:HA	1.74	0.45
1:I:150:GLU:HG3	1:I:153:ASP:HB3	1.98	0.45
1:D:178:LEU:HD12	1:D:178:LEU:HA	1.83	0.45
1:J:17:SER:HA	1:J:144:ASP:O	2.16	0.45
1:J:117:ARG:O	1:J:260:THR:HA	2.16	0.45
1:J:231:ARG:HB3	1:J:280:ILE:HD13	1.98	0.45
1:B:163:ARG:HD3	1:B:163:ARG:HA	1.74	0.45
1:H:55:PRO:HB3	1:H:95:PHE:CD1	2.52	0.45
1:C:117:ARG:O	1:C:260:THR:HA	2.17	0.45
1:J:19:PHE:CE2	1:J:146:GLN:HG3	2.51	0.44
1:C:147:VAL:HG21	1:C:195:ILE:HD13	1.99	0.44
1:F:99:ARG:NH2	1:G:181:VAL:HG21	2.32	0.44
1:A:185:GLN:H	1:A:185:GLN:HG3	1.48	0.44
1:C:166:ALA:HB2	1:C:195:ILE:HG12	1.98	0.44
1:E:11:PRO:HA	1:E:137:ASN:O	2.18	0.44
1:H:23:ILE:HD11	1:H:195:ILE:HD12	1.98	0.44
1:H:97:ASP:OD2	1:H:99:ARG:NH1	2.50	0.44
1:A:38:TYR:CZ	1:A:105:ARG:HD3	2.53	0.44
1:H:140:LEU:HD13	1:H:191:ILE:HG13	1.99	0.44
1:G:282:PHE:CZ	1:G:286:ARG:HG3	2.53	0.44
1:I:147:VAL:HG21	1:I:195:ILE:HD13	1.99	0.44
1:A:19:PHE:CE2	1:A:146:GLN:HG3	2.53	0.44
1:A:240:LEU:HD13	1:E:241:THR:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:145:ILE:HG13	1:D:166:ALA:HB3	2.00	0.44
1:E:147:VAL:HG21	1:E:195:ILE:HD13	2.00	0.44
1:G:221:SER:HB2	1:H:281:ILE:HD11	2.00	0.44
1:I:99:ARG:NH2	1:J:181:VAL:HG21	2.33	0.44
1:A:99:ARG:NH2	1:B:181:VAL:HG21	2.33	0.44
1:C:185:GLN:H	1:C:185:GLN:HG3	1.52	0.44
1:H:178:LEU:HD12	1:H:178:LEU:HA	1.76	0.44
1:B:155:GLU:O	1:B:161:TRP:NE1	2.48	0.43
1:E:119:PHE:HB3	1:E:120:PRO:HD3	2.01	0.43
1:F:36:ASP:HB2	1:F:107:LEU:HD13	2.00	0.43
1:F:93:MET:HB3	1:F:101:ILE:HB	1.99	0.43
1:E:38:TYR:CZ	1:E:105:ARG:HD3	2.54	0.43
1:E:118:LEU:HD12	1:E:118:LEU:H	1.84	0.43
1:F:210:LEU:HB3	1:F:211:PRO:HD3	2.01	0.43
1:I:166:ALA:HB2	1:I:195:ILE:HG12	2.00	0.43
1:I:253:LEU:HD12	1:I:253:LEU:HA	1.88	0.43
1:J:11:PRO:HA	1:J:137:ASN:O	2.18	0.43
1:A:55:PRO:HB3	1:A:95:PHE:CD1	2.54	0.43
1:F:119:PHE:HB3	1:F:120:PRO:HD3	2.01	0.43
1:F:58:VAL:HG13	1:F:62:GLN:HB3	2.01	0.43
1:F:97:ASP:OD2	1:F:99:ARG:NH1	2.51	0.43
1:C:38:TYR:CZ	1:C:105:ARG:HD3	2.54	0.43
1:E:178:LEU:HD12	1:E:178:LEU:HA	1.81	0.43
1:G:22:LYS:HE3	1:G:24:TYR:CD1	2.54	0.43
1:I:241:THR:HA	1:J:240:LEU:HD13	2.01	0.43
1:A:93:MET:HB3	1:A:101:ILE:HB	2.01	0.43
1:A:140:LEU:HD13	1:A:191:ILE:HG13	2.01	0.43
1:B:119:PHE:HB3	1:B:120:PRO:HD3	2.01	0.43
1:A:181:VAL:HG21	1:E:99:ARG:NH2	2.33	0.42
1:E:155:GLU:C	1:E:161:TRP:HE1	2.21	0.42
1:H:38:TYR:CZ	1:H:105:ARG:HD3	2.53	0.42
1:J:97:ASP:OD2	1:J:99:ARG:NH1	2.52	0.42
1:E:22:LYS:HE3	1:E:24:TYR:CD1	2.54	0.42
1:E:156:GLU:CD	1:E:156:GLU:H	2.22	0.42
1:J:282:PHE:CZ	1:J:286:ARG:HG3	2.54	0.42
1:F:162:ILE:HD13	1:F:197:ALA:HB2	2.01	0.42
1:G:20:ILE:HD12	1:G:195:ILE:HD11	2.00	0.42
1:H:185:GLN:H	1:H:185:GLN:HG3	1.52	0.42
1:I:119:PHE:HB3	1:I:120:PRO:HD3	2.01	0.42
1:I:178:LEU:HA	1:I:178:LEU:HD12	1.75	0.42
1:B:291:VAL:HG12	1:B:293:ASP:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:241:THR:HA	1:G:240:LEU:HD13	2.02	0.42
1:G:55:PRO:HB3	1:G:95:PHE:CD1	2.55	0.42
1:J:302:LEU:C	1:J:305:PRO:HD2	2.40	0.42
1:C:150:GLU:HG3	1:C:153:ASP:HB3	2.00	0.42
1:E:20:ILE:HD12	1:E:195:ILE:HD11	2.01	0.42
1:H:260:THR:H	1:H:263:ASP:HB2	1.84	0.42
1:I:145:ILE:HG13	1:I:166:ALA:HB3	2.01	0.42
1:F:185:GLN:H	1:F:185:GLN:HG3	1.56	0.42
1:A:117:ARG:O	1:A:260:THR:HA	2.20	0.42
1:I:55:PRO:HB3	1:I:95:PHE:CD1	2.55	0.42
1:A:134:SER:HB3	1:E:57:ILE:HD13	2.01	0.42
1:D:297:ILE:O	1:D:301:ARG:HB2	2.19	0.42
1:E:163:ARG:HD3	1:E:163:ARG:HA	1.75	0.42
1:F:130:LEU:HD23	1:F:130:LEU:HA	1.91	0.42
1:G:37:GLY:O	1:G:105:ARG:HD2	2.20	0.42
1:G:140:LEU:HD13	1:G:191:ILE:HG13	2.02	0.42
1:J:147:VAL:HG21	1:J:195:ILE:HD13	2.02	0.42
1:B:55:PRO:HB3	1:B:95:PHE:CD1	2.55	0.42
1:F:178:LEU:HD12	1:F:178:LEU:HA	1.78	0.42
1:G:42:GLN:HG3	1:G:101:ILE:HG12	2.01	0.42
1:I:185:GLN:H	1:I:185:GLN:HG3	1.51	0.42
1:C:119:PHE:HB3	1:C:120:PRO:HD3	2.01	0.42
1:H:204:TYR:O	1:H:208:PHE:HB2	2.19	0.42
1:J:300:CYS:O	1:J:304:PHE:HB2	2.20	0.42
1:A:118:LEU:HD12	1:A:118:LEU:H	1.85	0.41
1:B:165:LYS:HG3	1:I:163:ARG:HB3	2.01	0.41
1:E:130:LEU:HD23	1:E:130:LEU:HA	1.89	0.41
1:F:231:ARG:HB3	1:F:280:ILE:HD13	2.01	0.41
1:G:185:GLN:H	1:G:185:GLN:HG3	1.53	0.41
1:B:178:LEU:HD12	1:B:178:LEU:HA	1.78	0.41
1:C:140:LEU:HD13	1:C:191:ILE:HG13	2.02	0.41
1:D:155:GLU:O	1:D:161:TRP:NE1	2.53	0.41
1:G:119:PHE:HB3	1:G:120:PRO:HD3	2.01	0.41
1:J:55:PRO:HB3	1:J:95:PHE:CD1	2.56	0.41
1:C:92:LEU:HD23	1:C:92:LEU:HA	1.94	0.41
1:H:99:ARG:CZ	1:I:181:VAL:HG21	2.51	0.41
1:J:20:ILE:HD12	1:J:195:ILE:HD11	2.01	0.41
1:A:178:LEU:HD12	1:A:178:LEU:HA	1.79	0.41
1:C:148:TYR:HE2	1:D:177:HIS:HE2	1.68	0.41
1:I:11:PRO:HA	1:I:137:ASN:O	2.20	0.41
1:I:44:THR:HA	1:I:99:ARG:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:130:LEU:HD23	1:I:130:LEU:HA	1.90	0.41
1:B:42:GLN:HG3	1:B:101:ILE:HG12	2.03	0.41
1:C:241:THR:HA	1:D:240:LEU:HD13	2.03	0.41
1:D:117:ARG:O	1:D:260:THR:HA	2.20	0.41
1:E:37:GLY:O	1:E:105:ARG:HD2	2.21	0.41
1:J:119:PHE:HB3	1:J:120:PRO:HD3	2.03	0.41
1:A:200:ASN:HA	1:A:201:PRO:HD3	1.94	0.41
1:B:287:GLN:HG3	1:B:293:ASP:HB2	2.03	0.41
1:C:22:LYS:HE3	1:C:24:TYR:CD1	2.55	0.41
1:G:147:VAL:HG21	1:G:195:ILE:HD13	2.02	0.41
1:I:297:ILE:O	1:I:301:ARG:HB2	2.21	0.41
1:A:297:ILE:O	1:A:301:ARG:HB2	2.19	0.41
1:D:16:VAL:HA	1:D:40:VAL:O	2.21	0.41
1:D:14:VAL:HG22	1:D:43:TRP:HB3	2.03	0.41
1:B:185:GLN:H	1:B:185:GLN:HG3	1.49	0.41
1:F:134:SER:HB3	1:J:57:ILE:HD13	2.03	0.41
1:G:178:LEU:HD12	1:G:178:LEU:HA	1.79	0.41
1:H:42:GLN:HG3	1:H:101:ILE:HG12	2.03	0.41
1:I:140:LEU:HD13	1:I:191:ILE:HG13	2.03	0.41
1:B:169:HIS:HA	1:I:168:THR:O	2.19	0.41
1:C:20:ILE:HD12	1:C:195:ILE:HD11	2.02	0.41
1:E:205:LEU:HD23	1:E:209:ILE:HD12	2.03	0.41
1:G:224:TRP:CE2	1:G:301:ARG:HG2	2.56	0.41
1:A:92:LEU:HD23	1:A:92:LEU:HA	1.96	0.40
1:C:200:ASN:HA	1:C:201:PRO:HD3	1.92	0.40
1:E:287:GLN:CB	1:E:291:VAL:HB	2.51	0.40
1:F:20:ILE:HD12	1:F:195:ILE:HD11	2.02	0.40
1:J:163:ARG:HD3	1:J:163:ARG:HA	1.74	0.40
1:C:26:VAL:HG22	1:C:33:TYR:HB3	2.02	0.40
1:D:300:CYS:O	1:D:304:PHE:HB2	2.21	0.40
1:H:300:CYS:O	1:H:304:PHE:HB2	2.20	0.40
1:B:287:GLN:HB2	1:B:291:VAL:HB	2.03	0.40
1:E:282:PHE:CZ	1:E:286:ARG:HG3	2.57	0.40
1:F:155:GLU:O	1:F:161:TRP:NE1	2.52	0.40
1:H:145:ILE:HD12	1:H:168:THR:HG23	2.04	0.40
1:H:212:LEU:HD23	1:H:245:TYR:CD2	2.57	0.40
1:J:178:LEU:HD12	1:J:178:LEU:HA	1.79	0.40
1:E:185:GLN:H	1:E:185:GLN:HG3	1.53	0.40
1:F:221:SER:HB2	1:G:281:ILE:HD11	2.02	0.40
1:H:63:ILE:HD12	1:H:90:LYS:HG3	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	305/322 (95%)	284 (93%)	21 (7%)	0	100	100
1	B	305/322 (95%)	284 (93%)	21 (7%)	0	100	100
1	C	305/322 (95%)	284 (93%)	21 (7%)	0	100	100
1	D	305/322 (95%)	284 (93%)	21 (7%)	0	100	100
1	E	305/322 (95%)	283 (93%)	22 (7%)	0	100	100
1	F	305/322 (95%)	284 (93%)	21 (7%)	0	100	100
1	G	305/322 (95%)	284 (93%)	21 (7%)	0	100	100
1	H	305/322 (95%)	284 (93%)	21 (7%)	0	100	100
1	I	305/322 (95%)	284 (93%)	21 (7%)	0	100	100
1	J	305/322 (95%)	283 (93%)	22 (7%)	0	100	100
All	All	3050/3220 (95%)	2838 (93%)	212 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	274/283 (97%)	255 (93%)	19 (7%)	15	49
1	B	274/283 (97%)	257 (94%)	17 (6%)	18	53
1	C	274/283 (97%)	255 (93%)	19 (7%)	15	49
1	D	274/283 (97%)	254 (93%)	20 (7%)	14	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	274/283 (97%)	256 (93%)	18 (7%)	16	51
1	F	274/283 (97%)	256 (93%)	18 (7%)	16	51
1	G	274/283 (97%)	255 (93%)	19 (7%)	15	49
1	H	274/283 (97%)	255 (93%)	19 (7%)	15	49
1	I	274/283 (97%)	255 (93%)	19 (7%)	15	49
1	J	274/283 (97%)	255 (93%)	19 (7%)	15	49
All	All	2740/2830 (97%)	2553 (93%)	187 (7%)	16	49

All (187) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	VAL
1	A	65	ARG
1	A	118	LEU
1	A	123	ARG
1	A	130	LEU
1	A	138	GLN
1	A	144	ASP
1	A	145	ILE
1	A	150	GLU
1	A	151	ASN
1	A	156	GLU
1	A	185	GLN
1	A	212	LEU
1	A	247	PHE
1	A	253	LEU
1	A	289	ASN
1	A	296	LEU
1	A	301	ARG
1	A	304	PHE
1	B	16	VAL
1	B	118	LEU
1	B	123	ARG
1	B	130	LEU
1	B	138	GLN
1	B	144	ASP
1	B	145	ILE
1	B	150	GLU
1	B	151	ASN
1	B	156	GLU

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Mol	Chain	Res	Type
1	B	185	GLN
1	B	212	LEU
1	B	247	PHE
1	B	253	LEU
1	B	296	LEU
1	B	301	ARG
1	B	304	PHE
1	C	16	VAL
1	C	65	ARG
1	C	118	LEU
1	C	123	ARG
1	C	130	LEU
1	C	138	GLN
1	C	144	ASP
1	C	145	ILE
1	C	150	GLU
1	C	151	ASN
1	C	156	GLU
1	C	185	GLN
1	C	212	LEU
1	C	247	PHE
1	C	253	LEU
1	C	289	ASN
1	C	296	LEU
1	C	301	ARG
1	C	304	PHE
1	D	16	VAL
1	D	65	ARG
1	D	118	LEU
1	D	123	ARG
1	D	127	VAL
1	D	130	LEU
1	D	138	GLN
1	D	144	ASP
1	D	145	ILE
1	D	150	GLU
1	D	151	ASN
1	D	156	GLU
1	D	185	GLN
1	D	212	LEU
1	D	247	PHE
1	D	253	LEU

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Mol	Chain	Res	Type
1	D	289	ASN
1	D	296	LEU
1	D	301	ARG
1	D	304	PHE
1	E	16	VAL
1	E	118	LEU
1	E	123	ARG
1	E	127	VAL
1	E	130	LEU
1	E	138	GLN
1	E	144	ASP
1	E	145	ILE
1	E	150	GLU
1	E	151	ASN
1	E	156	GLU
1	E	185	GLN
1	E	212	LEU
1	E	247	PHE
1	E	253	LEU
1	E	296	LEU
1	E	301	ARG
1	E	304	PHE
1	F	16	VAL
1	F	65	ARG
1	F	118	LEU
1	F	123	ARG
1	F	130	LEU
1	F	138	GLN
1	F	145	ILE
1	F	150	GLU
1	F	151	ASN
1	F	156	GLU
1	F	185	GLN
1	F	212	LEU
1	F	247	PHE
1	F	253	LEU
1	F	289	ASN
1	F	296	LEU
1	F	301	ARG
1	F	304	PHE
1	G	16	VAL
1	G	118	LEU

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Mol	Chain	Res	Type
1	G	123	ARG
1	G	127	VAL
1	G	130	LEU
1	G	138	GLN
1	G	144	ASP
1	G	145	ILE
1	G	150	GLU
1	G	151	ASN
1	G	156	GLU
1	G	185	GLN
1	G	212	LEU
1	G	247	PHE
1	G	253	LEU
1	G	289	ASN
1	G	296	LEU
1	G	301	ARG
1	G	304	PHE
1	H	16	VAL
1	H	118	LEU
1	H	123	ARG
1	H	127	VAL
1	H	130	LEU
1	H	138	GLN
1	H	144	ASP
1	H	145	ILE
1	H	150	GLU
1	H	151	ASN
1	H	156	GLU
1	H	185	GLN
1	H	212	LEU
1	H	247	PHE
1	H	253	LEU
1	H	289	ASN
1	H	296	LEU
1	H	301	ARG
1	H	304	PHE
1	I	16	VAL
1	I	65	ARG
1	I	118	LEU
1	I	123	ARG
1	I	130	LEU
1	I	138	GLN

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Mol	Chain	Res	Type
1	I	144	ASP
1	I	145	ILE
1	I	150	GLU
1	I	151	ASN
1	I	156	GLU
1	I	185	GLN
1	I	212	LEU
1	I	247	PHE
1	I	253	LEU
1	I	289	ASN
1	I	296	LEU
1	I	301	ARG
1	I	304	PHE
1	J	16	VAL
1	J	65	ARG
1	J	118	LEU
1	J	123	ARG
1	J	130	LEU
1	J	138	GLN
1	J	144	ASP
1	J	145	ILE
1	J	150	GLU
1	J	151	ASN
1	J	156	GLU
1	J	185	GLN
1	J	212	LEU
1	J	247	PHE
1	J	253	LEU
1	J	289	ASN
1	J	296	LEU
1	J	301	ARG
1	J	304	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [i](#)

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	307/322 (95%)	-0.08	12 (3%)	39	25	48, 89, 175, 246	0
1	B	307/322 (95%)	0.09	13 (4%)	36	23	49, 81, 194, 258	0
1	C	307/322 (95%)	-0.03	19 (6%)	20	11	44, 84, 201, 252	0
1	D	307/322 (95%)	-0.01	11 (3%)	42	27	45, 84, 177, 271	0
1	E	307/322 (95%)	-0.13	9 (2%)	51	36	51, 87, 178, 325	0
1	F	307/322 (95%)	-0.04	21 (6%)	17	10	45, 86, 184, 276	0
1	G	307/322 (95%)	-0.05	13 (4%)	36	23	50, 80, 176, 262	0
1	H	307/322 (95%)	0.13	22 (7%)	15	9	45, 86, 201, 255	0
1	I	307/322 (95%)	-0.05	17 (5%)	25	14	46, 78, 181, 288	0
1	J	307/322 (95%)	0.00	14 (4%)	32	20	52, 84, 199, 282	0
All	All	3070/3220 (95%)	-0.02	151 (4%)	29	17	44, 84, 190, 325	0

All (151) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	151	ASN	13.9
1	E	289	ASN	11.5
1	H	153	ASP	11.1
1	H	152	ILE	10.9
1	J	181	VAL	10.0
1	C	180	SER	9.6
1	C	289	ASN	8.5
1	J	153	ASP	8.3
1	I	289	ASN	7.9
1	E	287	GLN	7.8
1	F	180	SER	7.6
1	J	52	GLY	7.0
1	B	180	SER	6.8

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Mol	Chain	Res	Type	RSRZ
1	A	153	ASP	6.6
1	C	181	VAL	6.5
1	B	289	ASN	6.4
1	E	153	ASP	6.2
1	A	152	ILE	5.9
1	E	288	ALA	5.9
1	H	289	ASN	5.9
1	G	315	LEU	5.8
1	H	180	SER	5.8
1	I	287	GLN	5.8
1	C	306	LEU	5.3
1	J	180	SER	5.3
1	H	290	GLY	5.2
1	B	152	ILE	5.1
1	J	304	PHE	5.1
1	E	290	GLY	5.0
1	J	152	ILE	5.0
1	G	289	ASN	4.9
1	D	180	SER	4.9
1	C	307	GLY	4.8
1	F	151	ASN	4.8
1	F	177	HIS	4.8
1	J	289	ASN	4.8
1	F	183	PRO	4.7
1	D	292	GLU	4.7
1	G	314	VAL	4.7
1	F	152	ILE	4.6
1	H	315	LEU	4.6
1	I	291	VAL	4.5
1	I	286	ARG	4.4
1	I	148	TYR	4.2
1	I	180	SER	4.2
1	G	180	SER	4.2
1	F	174	ARG	4.2
1	C	313	CYS	4.2
1	F	153	ASP	4.2
1	B	317	ILE	4.2
1	A	175	TYR	4.1
1	I	290	GLY	4.1
1	I	150	GLU	4.1
1	C	303	ALA	4.1
1	I	153	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
1	G	311	ILE	4.0
1	F	178	LEU	4.0
1	A	317	ILE	3.9
1	F	317	ILE	3.8
1	I	181	VAL	3.8
1	B	287	GLN	3.8
1	I	288	ALA	3.8
1	I	152	ILE	3.7
1	E	180	SER	3.7
1	A	151	ASN	3.6
1	H	179	SER	3.6
1	J	308	PHE	3.6
1	D	153	ASP	3.5
1	C	308	PHE	3.4
1	E	291	VAL	3.4
1	G	151	ASN	3.3
1	J	154	ASN	3.3
1	A	154	ASN	3.2
1	C	315	LEU	3.2
1	H	150	GLU	3.2
1	H	148	TYR	3.2
1	F	179	SER	3.1
1	I	179	SER	3.1
1	F	176	ASP	3.1
1	A	186	ASN	3.0
1	E	181	VAL	3.0
1	I	177	HIS	3.0
1	B	179	SER	3.0
1	F	288	ALA	3.0
1	C	179	SER	3.0
1	G	313	CYS	2.9
1	A	176	ASP	2.9
1	C	302	LEU	2.9
1	C	309	LEU	2.9
1	F	299	ARG	2.9
1	I	285	HIS	2.8
1	J	156	GLU	2.8
1	H	181	VAL	2.8
1	B	290	GLY	2.8
1	B	300	CYS	2.7
1	C	305	PRO	2.7
1	C	153	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	G	153	ASP	2.7
1	H	139	GLN	2.7
1	C	317	ILE	2.6
1	F	315	LEU	2.6
1	G	310	ALA	2.6
1	I	182	GLN	2.6
1	F	49	LYS	2.5
1	H	164	GLY	2.5
1	A	180	SER	2.5
1	J	177	HIS	2.5
1	G	152	ILE	2.5
1	C	49	LYS	2.5
1	G	304	PHE	2.5
1	A	188	PHE	2.5
1	F	185	GLN	2.5
1	H	291	VAL	2.4
1	J	183	PRO	2.4
1	C	304	PHE	2.4
1	D	295	LEU	2.4
1	B	286	ARG	2.4
1	D	177	HIS	2.4
1	A	315	LEU	2.4
1	F	289	ASN	2.4
1	H	302	LEU	2.4
1	C	314	VAL	2.4
1	E	315	LEU	2.3
1	H	304	PHE	2.3
1	D	179	SER	2.3
1	D	286	ARG	2.3
1	F	290	GLY	2.3
1	G	305	PRO	2.3
1	F	175	TYR	2.3
1	H	11	PRO	2.3
1	J	305	PRO	2.2
1	A	150	GLU	2.2
1	B	315	LEU	2.2
1	H	314	VAL	2.2
1	C	288	ALA	2.2
1	F	287	GLN	2.2
1	B	150	GLU	2.2
1	D	181	VAL	2.1
1	J	173	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	I	315	LEU	2.1
1	B	223	PHE	2.1
1	H	308	PHE	2.1
1	F	186	ASN	2.1
1	D	315	LEU	2.1
1	D	289	ASN	2.1
1	H	156	GLU	2.1
1	H	311	ILE	2.1
1	G	312	GLY	2.1
1	D	290	GLY	2.0
1	B	294	ASP	2.0
1	H	53	ASP	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 monosaccharides 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.