



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:26 AM UTC

PDB ID : 3HZR / pdb_00003hzh
Title : Tryptophanyl-tRNA synthetase homolog from *Entamoeba histolytica*
Authors : Arakaki, T.; Merritt, E.A.; Medical Structural Genomics of Pathogenic Protozoa (MSGPP)
Deposited on : 2009-06-24
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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

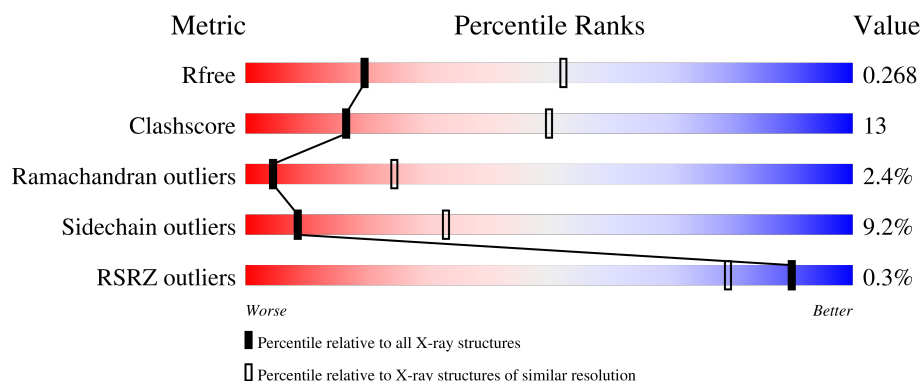
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	386	 69% 22% 6% .
1	B	386	 70% 19% 7% .
1	C	386	 69% 20% 7% .
1	D	386	 70% 20% 6% .
1	E	386	 72% 19% 6% .

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Mol	Chain	Length	Quality of chain
1	F	386	71% 19% 6% ••

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17738 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 Tryptophanyl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	0	0	0
			2958	1905	479	565	9			
1	B	374	Total	C	N	O	S	0	0	0
			2954	1903	479	563	9			
1	C	374	Total	C	N	O	S	0	0	0
			2957	1906	479	563	9			
1	D	374	Total	C	N	O	S	0	0	0
			2958	1905	479	565	9			
1	E	374	Total	C	N	O	S	0	0	0
			2954	1903	479	563	9			
1	F	374	Total	C	N	O	S	0	0	0
			2957	1906	479	563	9			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	expression tag	PDB 3HZR
A	-7	ALA	-	expression tag	PDB 3HZR
A	-6	HIS	-	expression tag	PDB 3HZR
A	-5	HIS	-	expression tag	PDB 3HZR
A	-4	HIS	-	expression tag	PDB 3HZR
A	-3	HIS	-	expression tag	PDB 3HZR
A	-2	HIS	-	expression tag	PDB 3HZR
A	-1	HIS	-	expression tag	PDB 3HZR
B	-8	MET	-	expression tag	PDB 3HZR
B	-7	ALA	-	expression tag	PDB 3HZR
B	-6	HIS	-	expression tag	PDB 3HZR
B	-5	HIS	-	expression tag	PDB 3HZR
B	-4	HIS	-	expression tag	PDB 3HZR
B	-3	HIS	-	expression tag	PDB 3HZR
B	-2	HIS	-	expression tag	PDB 3HZR
B	-1	HIS	-	expression tag	PDB 3HZR
C	-8	MET	-	expression tag	PDB 3HZR

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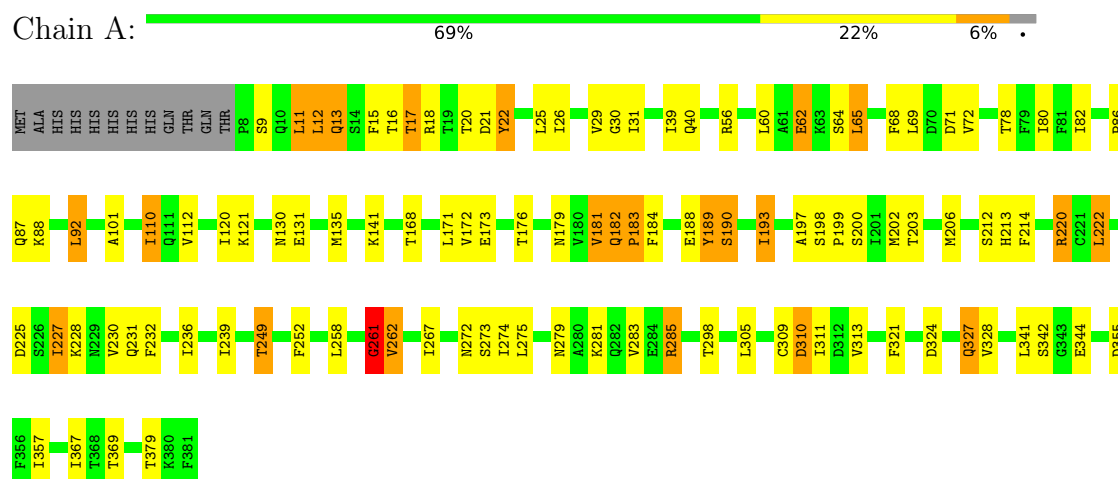
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	ALA	-	expression tag	PDB 3HZR
C	-6	HIS	-	expression tag	PDB 3HZR
C	-5	HIS	-	expression tag	PDB 3HZR
C	-4	HIS	-	expression tag	PDB 3HZR
C	-3	HIS	-	expression tag	PDB 3HZR
C	-2	HIS	-	expression tag	PDB 3HZR
C	-1	HIS	-	expression tag	PDB 3HZR
D	-8	MET	-	expression tag	PDB 3HZR
D	-7	ALA	-	expression tag	PDB 3HZR
D	-6	HIS	-	expression tag	PDB 3HZR
D	-5	HIS	-	expression tag	PDB 3HZR
D	-4	HIS	-	expression tag	PDB 3HZR
D	-3	HIS	-	expression tag	PDB 3HZR
D	-2	HIS	-	expression tag	PDB 3HZR
D	-1	HIS	-	expression tag	PDB 3HZR
E	-8	MET	-	expression tag	PDB 3HZR
E	-7	ALA	-	expression tag	PDB 3HZR
E	-6	HIS	-	expression tag	PDB 3HZR
E	-5	HIS	-	expression tag	PDB 3HZR
E	-4	HIS	-	expression tag	PDB 3HZR
E	-3	HIS	-	expression tag	PDB 3HZR
E	-2	HIS	-	expression tag	PDB 3HZR
E	-1	HIS	-	expression tag	PDB 3HZR
F	-8	MET	-	expression tag	PDB 3HZR
F	-7	ALA	-	expression tag	PDB 3HZR
F	-6	HIS	-	expression tag	PDB 3HZR
F	-5	HIS	-	expression tag	PDB 3HZR
F	-4	HIS	-	expression tag	PDB 3HZR
F	-3	HIS	-	expression tag	PDB 3HZR
F	-2	HIS	-	expression tag	PDB 3HZR
F	-1	HIS	-	expression tag	PDB 3HZR

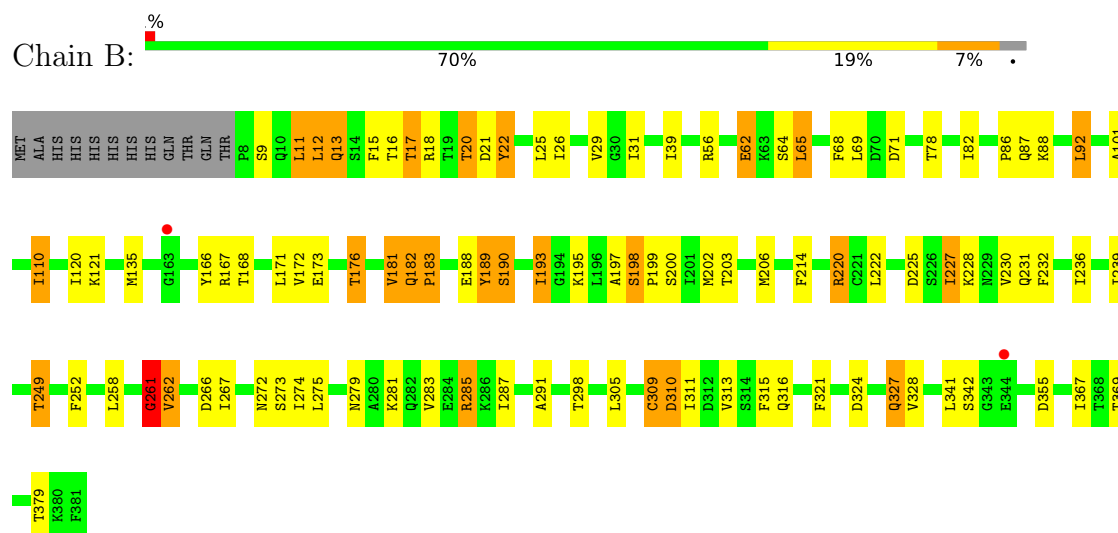
3 Residue-property plots

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: Tryptophanyl-tRNA synthetase

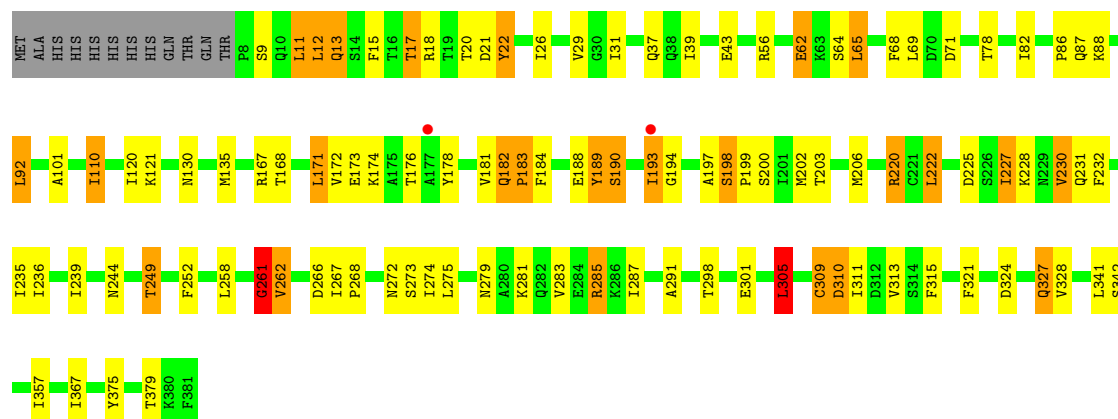


• Molecule 1: Tryptophanyl-tRNA synthetase



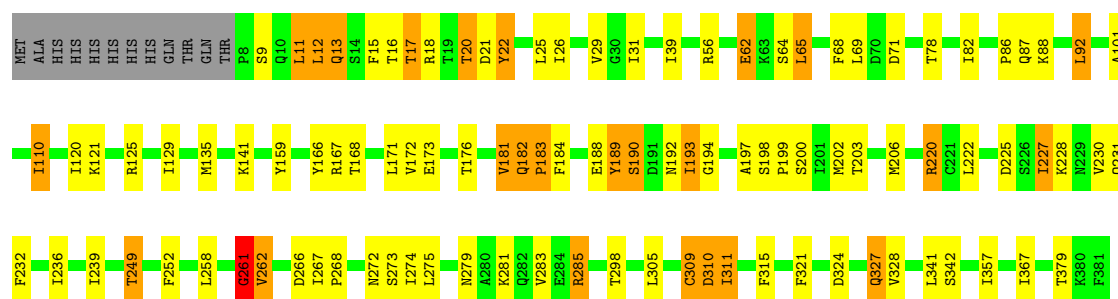
• Molecule 1: Tryptophanyl-tRNA synthetase





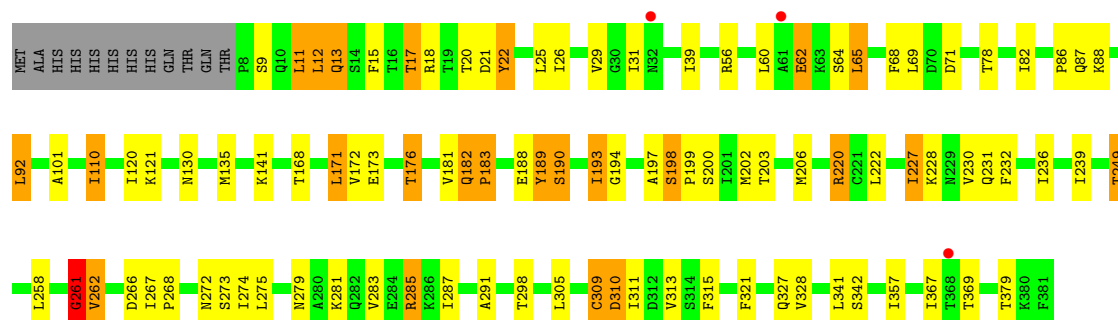
• Molecule 1: Tryptophanyl-tRNA synthetase

Chain D: 70% 20% 6% .



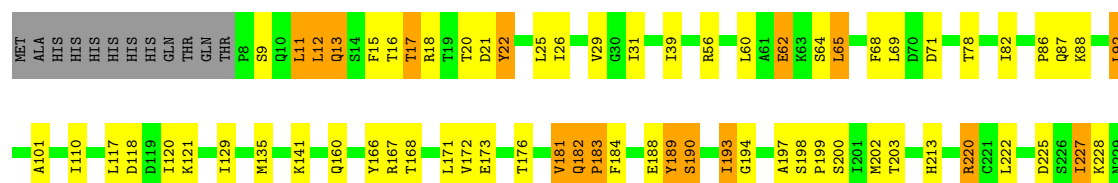
• Molecule 1: Tryptophanyl-tRNA synthetase

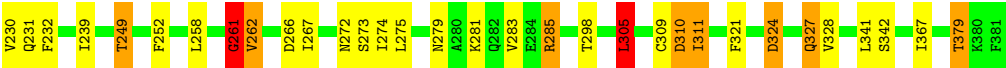
Chain E: 72% 19% 6% .



• Molecule 1: Tryptophanyl-tRNA synthetase

Chain F: 71% 19% 6% .





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.20Å 158.88Å 100.28Å 90.00° 107.33° 90.00°	Depositor
Resolution (Å)	47.89 – 3.00 47.89 – 3.00	Depositor EDS
% Data completeness (in resolution range)	97.6 (47.89-3.00) 97.6 (47.89-3.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 3.01Å)	Xtriage
Refinement program	REFMAC refmac_5.5.0089	Depositor
R, R_{free}	0.228 , 0.250 (Not available) , 0.268	Depositor DCC
R_{free} test set	2753 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	80.9	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	17738	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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	0.79	0/3019	0.96	5/4084 (0.1%)
1	B	0.79	0/3015	0.95	5/4079 (0.1%)
1	C	0.71	1/3018 (0.0%)	0.93	7/4083 (0.2%)
1	D	0.78	0/3019	0.95	6/4084 (0.1%)
1	E	0.65	0/3015	0.91	5/4079 (0.1%)
1	F	0.76	1/3018 (0.0%)	0.96	6/4083 (0.1%)
All	All	0.75	2/18104 (0.0%)	0.95	34/24492 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2
1	D	0	2
1	E	0	2
1	F	0	2
All	All	0	12

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	160	GLN	CG-CD	5.09	1.64	1.52
1	C	305	LEU	CG-CD2	5.05	1.69	1.52

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	15	PHE	N-CA-C	7.22	120.91	109.50
1	A	15	PHE	N-CA-C	7.03	120.61	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	15	PHE	N-CA-C	7.03	120.41	109.52
1	B	15	PHE	N-CA-C	6.97	120.52	109.50
1	F	15	PHE	N-CA-C	6.90	120.40	109.50
1	E	15	PHE	N-CA-C	6.84	120.13	109.52
1	B	190	SER	N-CA-C	-6.22	105.52	113.23
1	F	261	GLY	N-CA-C	-5.98	99.00	113.18
1	F	311	ILE	CB-CA-C	-5.81	104.35	110.62
1	D	261	GLY	N-CA-C	-5.79	99.46	113.18
1	D	190	SER	N-CA-C	-5.78	106.23	113.28
1	C	190	SER	N-CA-C	-5.76	106.09	113.23
1	C	261	GLY	N-CA-C	-5.73	99.60	113.18
1	F	190	SER	N-CA-C	-5.72	106.13	113.23
1	F	261	GLY	CA-C-N	5.64	131.85	121.70
1	F	261	GLY	C-N-CA	5.64	131.85	121.70
1	A	190	SER	N-CA-C	-5.64	106.24	113.23
1	D	311	ILE	CB-CA-C	-5.61	104.56	110.62
1	D	261	GLY	CA-C-N	5.59	131.76	121.70
1	D	261	GLY	C-N-CA	5.59	131.76	121.70
1	A	261	GLY	N-CA-C	-5.55	100.04	113.18
1	C	261	GLY	CA-C-N	5.47	131.55	121.70
1	C	261	GLY	C-N-CA	5.47	131.55	121.70
1	B	261	GLY	CA-C-N	5.46	131.53	121.70
1	B	261	GLY	C-N-CA	5.46	131.53	121.70
1	E	261	GLY	CA-C-N	5.45	131.51	121.70
1	E	261	GLY	C-N-CA	5.45	131.51	121.70
1	E	190	SER	N-CA-C	-5.44	106.49	113.23
1	A	261	GLY	CA-C-N	5.43	131.48	121.70
1	A	261	GLY	C-N-CA	5.43	131.48	121.70
1	B	261	GLY	N-CA-C	-5.38	100.44	113.18
1	E	261	GLY	N-CA-C	-5.10	101.09	113.18
1	C	230	VAL	CB-CA-C	-5.08	105.39	112.04
1	C	235	ILE	N-CA-C	-5.07	105.76	110.53

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	261	GLY	Peptide
1	A	309	CYS	Peptide
1	B	261	GLY	Peptide
1	B	309	CYS	Peptide
1	C	261	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	C	309	CYS	Peptide
1	D	261	GLY	Peptide
1	D	309	CYS	Peptide
1	E	261	GLY	Peptide
1	E	309	CYS	Peptide
1	F	261	GLY	Peptide
1	F	309	CYS	Peptide

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	2958	0	2910	82	4
1	B	2954	0	2906	73	2
1	C	2957	0	2915	93	3
1	D	2958	0	2910	87	1
1	E	2954	0	2906	76	0
1	F	2957	0	2915	80	2
All	All	17738	0	17462	454	6

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (454) 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:29:VAL:HG11	1:B:230:VAL:HG11	1.24	1.16
1:F:29:VAL:HG11	1:F:230:VAL:HG11	1.34	1.08
1:E:29:VAL:HG11	1:E:230:VAL:HG11	1.32	1.07
1:C:29:VAL:HG11	1:C:230:VAL:HG11	1.34	1.05
1:A:29:VAL:HG11	1:A:230:VAL:HG11	1.33	1.03
1:D:29:VAL:HG11	1:D:230:VAL:HG11	1.38	1.00
1:C:197:ALA:HA	1:D:193:ILE:HG23	1.47	0.96
1:B:87:GLN:C	1:B:135:MET:HE2	1.91	0.96
1:C:87:GLN:C	1:C:135:MET:HE2	1.91	0.94
1:A:87:GLN:C	1:A:135:MET:HE2	1.95	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:87:GLN:C	1:E:135:MET:HE2	1.99	0.87
1:B:29:VAL:CG1	1:B:230:VAL:HG11	2.05	0.87
1:E:197:ALA:HA	1:F:193:ILE:HG23	1.56	0.86
1:C:120:ILE:HD13	1:C:202:MET:HE2	1.57	0.86
1:E:120:ILE:HD13	1:E:202:MET:HE2	1.60	0.83
1:D:87:GLN:C	1:D:135:MET:HE2	2.02	0.83
1:E:197:ALA:HA	1:F:193:ILE:CG2	2.10	0.80
1:A:199:PRO:O	1:A:203:THR:HG23	1.80	0.80
1:F:87:GLN:C	1:F:135:MET:HE2	2.07	0.80
1:A:29:VAL:CG1	1:A:230:VAL:HG11	2.13	0.79
1:D:199:PRO:O	1:D:203:THR:HG23	1.83	0.78
1:B:29:VAL:HG11	1:B:230:VAL:CG1	2.11	0.76
1:C:29:VAL:CG1	1:C:230:VAL:HG11	2.15	0.76
1:E:29:VAL:CG1	1:E:230:VAL:HG11	2.13	0.76
1:C:197:ALA:HA	1:D:193:ILE:CG2	2.15	0.76
1:D:120:ILE:HD13	1:D:202:MET:HE2	1.67	0.75
1:B:88:LYS:N	1:B:135:MET:CE	2.50	0.75
1:C:11:LEU:HD12	1:C:12:LEU:N	2.03	0.74
1:D:227:ILE:O	1:D:230:VAL:HG23	1.87	0.74
1:A:197:ALA:HA	1:B:193:ILE:HG23	1.69	0.73
1:B:11:LEU:HD12	1:B:12:LEU:N	2.03	0.73
1:F:120:ILE:HD13	1:F:202:MET:HE2	1.70	0.73
1:B:120:ILE:HD13	1:B:202:MET:HE2	1.68	0.73
1:E:171:LEU:HD13	1:F:129:ILE:HD11	1.71	0.72
1:F:29:VAL:CG1	1:F:230:VAL:HG11	2.16	0.72
1:A:227:ILE:O	1:A:230:VAL:HG23	1.88	0.72
1:A:88:LYS:N	1:A:135:MET:CE	2.52	0.72
1:F:367:ILE:HG22	1:F:367:ILE:O	1.87	0.72
1:A:120:ILE:HD13	1:A:202:MET:HE2	1.70	0.72
1:F:11:LEU:HD12	1:F:12:LEU:N	2.05	0.72
1:F:29:VAL:HG11	1:F:230:VAL:CG1	2.17	0.72
1:C:88:LYS:N	1:C:135:MET:CE	2.53	0.71
1:B:172:VAL:O	1:B:176:THR:HG23	1.90	0.71
1:F:172:VAL:O	1:F:176:THR:HG23	1.90	0.71
1:E:193:ILE:HG23	1:F:197:ALA:HA	1.71	0.71
1:A:214:PHE:C	1:C:130:ASN:ND2	2.49	0.71
1:E:29:VAL:HG11	1:E:230:VAL:CG1	2.18	0.71
1:D:11:LEU:HD12	1:D:12:LEU:N	2.07	0.70
1:F:227:ILE:O	1:F:230:VAL:HG23	1.90	0.70
1:A:29:VAL:HG11	1:A:230:VAL:CG1	2.19	0.70
1:B:367:ILE:O	1:B:367:ILE:HG22	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:199:PRO:O	1:B:203:THR:HG23	1.92	0.69
1:A:11:LEU:HD12	1:A:12:LEU:N	2.07	0.69
1:E:199:PRO:O	1:E:203:THR:HG23	1.93	0.69
1:E:11:LEU:HD12	1:E:12:LEU:N	2.08	0.69
1:E:18:ARG:NH2	1:E:310:ASP:OD2	2.26	0.69
1:E:227:ILE:O	1:E:230:VAL:HG23	1.92	0.68
1:F:18:ARG:NH2	1:F:310:ASP:OD2	2.26	0.68
1:B:227:ILE:O	1:B:230:VAL:HG23	1.94	0.68
1:A:18:ARG:NH2	1:A:310:ASP:OD2	2.27	0.68
1:A:193:ILE:HG23	1:B:197:ALA:HA	1.75	0.68
1:E:88:LYS:N	1:E:135:MET:CE	2.57	0.68
1:F:199:PRO:O	1:F:203:THR:HG23	1.93	0.68
1:B:11:LEU:O	1:B:13:GLN:N	2.26	0.67
1:D:18:ARG:NH2	1:D:310:ASP:OD2	2.27	0.67
1:C:227:ILE:O	1:C:230:VAL:HG23	1.94	0.67
1:D:88:LYS:N	1:D:135:MET:CE	2.57	0.66
1:A:11:LEU:O	1:A:13:GLN:N	2.26	0.66
1:D:11:LEU:O	1:D:13:GLN:N	2.27	0.66
1:C:18:ARG:NH2	1:C:310:ASP:OD2	2.28	0.66
1:C:193:ILE:HG23	1:D:197:ALA:HA	1.77	0.66
1:B:18:ARG:NH2	1:B:310:ASP:OD2	2.29	0.66
1:D:29:VAL:CG1	1:D:230:VAL:HG11	2.19	0.66
1:C:267:ILE:O	1:C:272:ASN:ND2	2.30	0.65
1:B:65:LEU:HD22	1:B:69:LEU:CD1	2.27	0.64
1:C:21:ASP:O	1:C:22:TYR:HB2	1.97	0.64
1:D:172:VAL:O	1:D:176:THR:HG23	1.95	0.64
1:E:193:ILE:CG2	1:F:197:ALA:HA	2.26	0.64
1:C:88:LYS:N	1:C:135:MET:HE2	2.13	0.64
1:C:199:PRO:O	1:C:203:THR:HG23	1.98	0.64
1:C:29:VAL:HG11	1:C:230:VAL:CG1	2.20	0.64
1:B:88:LYS:N	1:B:135:MET:HE2	2.11	0.64
1:C:64:SER:HB2	1:C:249:THR:HG22	1.79	0.64
1:C:65:LEU:HD22	1:C:69:LEU:CD1	2.26	0.64
1:E:367:ILE:O	1:E:367:ILE:HG22	1.97	0.64
1:F:65:LEU:HD22	1:F:69:LEU:CD1	2.28	0.64
1:D:367:ILE:HG22	1:D:367:ILE:O	1.95	0.63
1:D:29:VAL:HG11	1:D:230:VAL:CG1	2.22	0.63
1:A:21:ASP:O	1:A:22:TYR:HB2	1.97	0.63
1:A:267:ILE:O	1:A:272:ASN:ND2	2.32	0.63
1:F:11:LEU:O	1:F:13:GLN:N	2.32	0.63
1:F:88:LYS:N	1:F:135:MET:CE	2.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:65:LEU:HD22	1:E:69:LEU:CD1	2.29	0.62
1:A:367:ILE:HG22	1:A:367:ILE:O	1.98	0.62
1:D:11:LEU:C	1:D:13:GLN:H	2.07	0.62
1:E:267:ILE:O	1:E:272:ASN:ND2	2.32	0.62
1:C:172:VAL:O	1:C:176:THR:HG23	1.99	0.62
1:D:176:THR:HG22	1:D:239:ILE:CD1	2.29	0.62
1:A:193:ILE:CG2	1:B:197:ALA:HA	2.30	0.62
1:E:172:VAL:O	1:E:176:THR:HG23	1.99	0.61
1:A:176:THR:HG22	1:A:239:ILE:CD1	2.30	0.61
1:E:64:SER:HB2	1:E:249:THR:HG22	1.82	0.61
1:B:11:LEU:C	1:B:13:GLN:H	2.07	0.61
1:C:87:GLN:HG2	1:C:121:LYS:NZ	2.16	0.61
1:E:11:LEU:O	1:E:13:GLN:N	2.31	0.61
1:C:174:LYS:HE3	1:D:125:ARG:HA	1.82	0.61
1:A:11:LEU:C	1:A:13:GLN:H	2.08	0.61
1:F:11:LEU:C	1:F:13:GLN:H	2.08	0.61
1:F:88:LYS:N	1:F:135:MET:HE2	2.15	0.61
1:E:26:ILE:HG23	1:E:31:ILE:O	2.01	0.61
1:B:87:GLN:C	1:B:135:MET:CE	2.70	0.60
1:D:267:ILE:O	1:D:272:ASN:ND2	2.35	0.60
1:A:65:LEU:HD22	1:A:69:LEU:CD1	2.31	0.60
1:E:11:LEU:C	1:E:13:GLN:H	2.09	0.60
1:E:21:ASP:O	1:E:22:TYR:HB2	2.01	0.60
1:C:87:GLN:C	1:C:135:MET:CE	2.72	0.60
1:F:64:SER:HB2	1:F:249:THR:HG22	1.84	0.59
1:F:21:ASP:O	1:F:22:TYR:HB2	2.01	0.59
1:A:197:ALA:HA	1:B:193:ILE:CG2	2.32	0.59
1:D:65:LEU:HD22	1:D:69:LEU:CD1	2.32	0.59
1:A:88:LYS:N	1:A:135:MET:HE2	2.12	0.59
1:B:21:ASP:O	1:B:22:TYR:HB2	2.03	0.59
1:C:173:GLU:HB3	1:D:194:GLY:HA3	1.83	0.59
1:C:367:ILE:HG22	1:C:367:ILE:O	2.03	0.59
1:F:176:THR:HG22	1:F:239:ILE:CD1	2.33	0.59
1:A:172:VAL:O	1:A:176:THR:HG23	2.02	0.58
1:D:21:ASP:O	1:D:22:TYR:HB2	2.03	0.58
1:E:71:ASP:OD1	1:E:220:ARG:HG3	2.03	0.58
1:E:88:LYS:N	1:E:135:MET:HE2	2.15	0.58
1:B:267:ILE:O	1:B:272:ASN:ND2	2.36	0.58
1:C:176:THR:HG22	1:C:239:ILE:CD1	2.34	0.58
1:D:88:LYS:N	1:D:135:MET:HE2	2.19	0.58
1:B:64:SER:HB2	1:B:249:THR:HG22	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:11:LEU:C	1:C:13:GLN:H	2.11	0.58
1:D:64:SER:HB2	1:D:249:THR:HG22	1.86	0.58
1:C:26:ILE:HG23	1:C:31:ILE:O	2.04	0.58
1:A:26:ILE:HG23	1:A:31:ILE:O	2.03	0.57
1:C:71:ASP:OD1	1:C:220:ARG:HG3	2.04	0.57
1:F:267:ILE:O	1:F:272:ASN:ND2	2.37	0.57
1:D:258:LEU:HD22	1:D:272:ASN:HB3	1.87	0.57
1:C:11:LEU:O	1:C:13:GLN:N	2.35	0.56
1:A:71:ASP:OD1	1:A:220:ARG:HG3	2.06	0.55
1:E:87:GLN:HG2	1:E:121:LYS:NZ	2.21	0.55
1:E:176:THR:HG22	1:E:239:ILE:CD1	2.37	0.55
1:F:87:GLN:HG2	1:F:121:LYS:NZ	2.21	0.55
1:F:62:GLU:HG3	1:F:65:LEU:HB2	1.89	0.55
1:C:301:GLU:O	1:C:305:LEU:HB2	2.07	0.55
1:B:92:LEU:HD22	1:B:321:PHE:CZ	2.42	0.55
1:B:285:ARG:CG	1:B:285:ARG:HH11	2.19	0.55
1:D:173:GLU:HG2	1:D:200:SER:OG	2.07	0.55
1:A:285:ARG:HH11	1:A:285:ARG:CG	2.21	0.54
1:B:87:GLN:HG2	1:B:121:LYS:NZ	2.23	0.54
1:D:71:ASP:OD1	1:D:220:ARG:HG3	2.07	0.54
1:D:274:ILE:HD13	1:D:283:VAL:HG13	1.90	0.54
1:A:78:THR:OG1	1:A:110:ILE:HD11	2.08	0.54
1:A:279:ASN:ND2	1:A:281:LYS:HE3	2.22	0.54
1:B:26:ILE:HG23	1:B:31:ILE:O	2.07	0.54
1:D:62:GLU:HG3	1:D:65:LEU:HB2	1.89	0.53
1:B:62:GLU:HG3	1:B:65:LEU:HB2	1.90	0.53
1:B:71:ASP:OD1	1:B:220:ARG:HG3	2.09	0.53
1:C:92:LEU:HD22	1:C:321:PHE:CZ	2.44	0.53
1:A:62:GLU:HG3	1:A:65:LEU:HB2	1.91	0.53
1:F:25:LEU:HD12	1:F:29:VAL:HG23	1.91	0.53
1:C:285:ARG:HH11	1:C:285:ARG:CG	2.22	0.53
1:E:92:LEU:HD22	1:E:321:PHE:CZ	2.44	0.53
1:E:285:ARG:HH11	1:E:285:ARG:CG	2.22	0.53
1:F:9:SER:H	1:F:231:GLN:HE22	1.57	0.53
1:F:258:LEU:HD22	1:F:272:ASN:HB3	1.90	0.52
1:A:92:LEU:HD22	1:A:321:PHE:CZ	2.44	0.52
1:C:261:GLY:HA2	1:C:262:VAL:HG23	1.91	0.52
1:D:87:GLN:HG2	1:D:121:LYS:NZ	2.23	0.52
1:F:26:ILE:HG23	1:F:31:ILE:O	2.09	0.52
1:E:274:ILE:HD13	1:E:283:VAL:HG13	1.91	0.52
1:D:176:THR:HG22	1:D:239:ILE:HD11	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:86:PRO:O	1:E:121:LYS:HD3	2.09	0.52
1:B:29:VAL:CG1	1:B:230:VAL:CG1	2.81	0.52
1:B:195:LYS:O	1:B:198:SER:OG	2.24	0.52
1:F:78:THR:HG22	1:F:220:ARG:HB2	1.91	0.52
1:A:64:SER:HB2	1:A:249:THR:HG22	1.92	0.52
1:E:78:THR:HG22	1:E:220:ARG:HB2	1.92	0.52
1:D:92:LEU:HD22	1:D:321:PHE:CZ	2.45	0.52
1:C:174:LYS:CE	1:D:125:ARG:HA	2.40	0.52
1:A:206:MET:SD	1:A:236:ILE:HD13	2.49	0.51
1:A:261:GLY:HA2	1:A:262:VAL:HG23	1.91	0.51
1:E:261:GLY:HA2	1:E:262:VAL:HG23	1.90	0.51
1:A:68:PHE:HB2	1:A:249:THR:HG21	1.91	0.51
1:E:62:GLU:HG3	1:E:65:LEU:HB2	1.92	0.51
1:F:68:PHE:HB2	1:F:249:THR:HG21	1.92	0.51
1:C:193:ILE:CG2	1:D:197:ALA:HA	2.39	0.51
1:A:78:THR:HG22	1:A:220:ARG:HB2	1.93	0.51
1:B:258:LEU:HD22	1:B:272:ASN:HB3	1.91	0.51
1:B:285:ARG:HH11	1:B:285:ARG:HG2	1.75	0.51
1:D:68:PHE:HB2	1:D:249:THR:HG21	1.93	0.51
1:C:87:GLN:HG2	1:C:121:LYS:HZ3	1.75	0.51
1:E:197:ALA:HA	1:F:193:ILE:HG21	1.92	0.51
1:C:274:ILE:HD13	1:C:283:VAL:HG13	1.92	0.51
1:A:258:LEU:HD22	1:A:272:ASN:HB3	1.92	0.51
1:B:261:GLY:HA2	1:B:262:VAL:HG23	1.91	0.51
1:C:62:GLU:HG3	1:C:65:LEU:HB2	1.93	0.51
1:E:82:ILE:HD11	1:E:101:ALA:HB2	1.93	0.51
1:F:285:ARG:HH11	1:F:285:ARG:CG	2.23	0.50
1:A:176:THR:HG22	1:A:239:ILE:HD11	1.92	0.50
1:B:279:ASN:ND2	1:B:281:LYS:HE3	2.25	0.50
1:F:188:GLU:O	1:F:189:TYR:CD2	2.65	0.50
1:A:87:GLN:HG2	1:A:121:LYS:NZ	2.27	0.50
1:F:71:ASP:OD1	1:F:220:ARG:HG3	2.11	0.50
1:D:285:ARG:HH11	1:D:285:ARG:CG	2.23	0.50
1:B:176:THR:HG22	1:B:239:ILE:CD1	2.42	0.50
1:D:26:ILE:HG23	1:D:31:ILE:O	2.12	0.50
1:B:78:THR:HG22	1:B:220:ARG:HB2	1.94	0.50
1:C:258:LEU:HD22	1:C:272:ASN:HB3	1.93	0.49
1:A:130:ASN:ND2	1:F:213:HIS:O	2.41	0.49
1:A:285:ARG:HH11	1:A:285:ARG:HG2	1.77	0.49
1:F:87:GLN:HG2	1:F:121:LYS:HZ3	1.77	0.49
1:F:274:ILE:HD13	1:F:283:VAL:HG13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:206:MET:SD	1:B:236:ILE:HD13	2.53	0.49
1:C:188:GLU:O	1:C:189:TYR:CD2	2.65	0.49
1:C:197:ALA:HB2	1:D:197:ALA:HB2	1.94	0.49
1:E:197:ALA:CA	1:F:193:ILE:HG23	2.37	0.49
1:E:279:ASN:ND2	1:E:281:LYS:HE3	2.28	0.49
1:F:92:LEU:HD22	1:F:321:PHE:CZ	2.48	0.49
1:B:9:SER:H	1:B:231:GLN:HE22	1.59	0.49
1:F:261:GLY:HA2	1:F:262:VAL:HG23	1.95	0.49
1:C:167:ARG:HA	1:D:159:TYR:CE2	2.48	0.49
1:C:285:ARG:HH11	1:C:285:ARG:HG2	1.77	0.48
1:C:173:GLU:HG2	1:C:200:SER:OG	2.13	0.48
1:C:176:THR:HG22	1:C:239:ILE:HD11	1.95	0.48
1:D:182:GLN:N	1:D:183:PRO:CD	2.76	0.48
1:B:65:LEU:HD22	1:B:69:LEU:HD11	1.94	0.48
1:C:173:GLU:O	1:D:192:ASN:HB2	2.12	0.48
1:C:262:VAL:HG23	1:C:313:VAL:HG22	1.94	0.48
1:D:188:GLU:O	1:D:189:TYR:CD2	2.66	0.48
1:E:285:ARG:HH11	1:E:285:ARG:HG2	1.77	0.48
1:C:68:PHE:HB2	1:C:249:THR:HG21	1.95	0.48
1:E:78:THR:OG1	1:E:110:ILE:HD11	2.13	0.48
1:F:17:THR:O	1:F:18:ARG:HB3	2.14	0.48
1:F:173:GLU:HG2	1:F:200:SER:OG	2.14	0.48
1:B:166:TYR:O	1:B:167:ARG:C	2.56	0.48
1:A:92:LEU:HD22	1:A:321:PHE:CE1	2.48	0.48
1:A:222:LEU:C	1:A:222:LEU:HD12	2.39	0.48
1:B:68:PHE:HB2	1:B:249:THR:HG21	1.96	0.48
1:D:78:THR:HG22	1:D:220:ARG:HB2	1.94	0.48
1:F:324:ASP:OD1	1:F:327:GLN:HG2	2.13	0.48
1:E:198:SER:O	1:E:199:PRO:C	2.57	0.48
1:E:92:LEU:HD22	1:E:321:PHE:CE1	2.50	0.47
1:E:206:MET:SD	1:E:236:ILE:HD13	2.54	0.47
1:C:206:MET:SD	1:C:236:ILE:HD13	2.54	0.47
1:F:182:GLN:N	1:F:183:PRO:CD	2.77	0.47
1:C:78:THR:HG22	1:C:220:ARG:HB2	1.94	0.47
1:D:17:THR:O	1:D:18:ARG:HB3	2.13	0.47
1:F:176:THR:HG22	1:F:239:ILE:HD11	1.96	0.47
1:D:13:GLN:O	1:D:13:GLN:CG	2.61	0.47
1:E:203:THR:HG22	1:E:232:PHE:CZ	2.50	0.47
1:B:262:VAL:HG23	1:B:313:VAL:HG22	1.96	0.47
1:E:172:VAL:HG11	1:E:203:THR:OG1	2.14	0.47
1:B:82:ILE:HD11	1:B:101:ALA:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:25:LEU:HD12	1:D:29:VAL:HG23	1.96	0.47
1:A:87:GLN:CA	1:A:135:MET:HE2	2.45	0.47
1:C:92:LEU:HD22	1:C:321:PHE:CE1	2.49	0.47
1:C:279:ASN:ND2	1:C:281:LYS:HE3	2.29	0.47
1:D:261:GLY:HA2	1:D:262:VAL:HG23	1.96	0.47
1:D:324:ASP:OD1	1:D:327:GLN:HG2	2.15	0.47
1:E:68:PHE:HB2	1:E:249:THR:HG21	1.95	0.47
1:A:9:SER:H	1:A:231:GLN:HE22	1.61	0.47
1:C:65:LEU:HD22	1:C:69:LEU:HD11	1.95	0.47
1:E:173:GLU:HG2	1:E:200:SER:OG	2.14	0.47
1:C:86:PRO:O	1:C:121:LYS:HD3	2.15	0.47
1:B:182:GLN:N	1:B:183:PRO:CD	2.78	0.47
1:F:166:TYR:O	1:F:167:ARG:C	2.59	0.47
1:A:172:VAL:HG11	1:A:203:THR:OG1	2.15	0.46
1:B:203:THR:HG22	1:B:232:PHE:CZ	2.49	0.46
1:C:9:SER:H	1:C:231:GLN:HE22	1.62	0.46
1:A:86:PRO:O	1:A:121:LYS:HD3	2.15	0.46
1:A:225:ASP:O	1:A:252:PHE:HA	2.15	0.46
1:B:78:THR:OG1	1:B:110:ILE:HD11	2.14	0.46
1:B:87:GLN:CA	1:B:135:MET:HE2	2.46	0.46
1:D:285:ARG:HH11	1:D:285:ARG:HG2	1.81	0.46
1:A:56:ARG:CZ	1:A:328:VAL:HG21	2.46	0.46
1:B:287:ILE:O	1:B:291:ALA:HB3	2.16	0.46
1:B:56:ARG:CZ	1:B:328:VAL:HG21	2.46	0.46
1:E:287:ILE:O	1:E:291:ALA:HB3	2.16	0.46
1:F:285:ARG:HH11	1:F:285:ARG:HG2	1.81	0.46
1:B:92:LEU:HD22	1:B:321:PHE:CE1	2.51	0.46
1:A:17:THR:O	1:A:18:ARG:HB3	2.16	0.46
1:A:188:GLU:O	1:A:189:TYR:CD2	2.69	0.46
1:B:25:LEU:HD12	1:B:29:VAL:HG23	1.98	0.46
1:C:87:GLN:CA	1:C:135:MET:HE2	2.44	0.46
1:E:65:LEU:HD22	1:E:69:LEU:HD11	1.97	0.46
1:A:214:PHE:CA	1:C:130:ASN:ND2	2.79	0.46
1:D:87:GLN:HG2	1:D:121:LYS:HZ3	1.81	0.46
1:A:87:GLN:C	1:A:135:MET:CE	2.77	0.45
1:A:182:GLN:N	1:A:183:PRO:CD	2.79	0.45
1:A:324:ASP:OD1	1:A:327:GLN:HG2	2.16	0.45
1:C:193:ILE:HG22	1:C:194:GLY:N	2.31	0.45
1:E:87:GLN:HG2	1:E:121:LYS:HZ3	1.81	0.45
1:E:171:LEU:CD1	1:F:129:ILE:HD11	2.44	0.45
1:F:379:THR:O	1:F:379:THR:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:184:PHE:CZ	1:D:232:PHE:HB2	2.51	0.45
1:D:206:MET:SD	1:D:236:ILE:HD13	2.55	0.45
1:E:188:GLU:O	1:E:189:TYR:CD2	2.68	0.45
1:C:13:GLN:CG	1:C:13:GLN:O	2.64	0.45
1:C:78:THR:OG1	1:C:110:ILE:HD11	2.16	0.45
1:A:29:VAL:CG1	1:A:230:VAL:CG1	2.89	0.45
1:B:198:SER:O	1:B:199:PRO:C	2.58	0.45
1:C:203:THR:HG22	1:C:232:PHE:CZ	2.51	0.45
1:E:29:VAL:CG1	1:E:230:VAL:CG1	2.88	0.45
1:B:188:GLU:O	1:B:189:TYR:CD2	2.70	0.45
1:C:171:LEU:HD13	1:D:129:ILE:HD11	1.98	0.45
1:C:173:GLU:HB3	1:D:194:GLY:CA	2.47	0.45
1:D:11:LEU:C	1:D:13:GLN:N	2.74	0.45
1:A:30:GLY:O	1:A:31:ILE:HG23	2.17	0.45
1:B:17:THR:O	1:B:18:ARG:HB3	2.17	0.45
1:A:87:GLN:HG2	1:A:121:LYS:HZ3	1.82	0.45
1:C:172:VAL:HG11	1:C:203:THR:OG1	2.17	0.45
1:D:203:THR:HG22	1:D:232:PHE:CZ	2.52	0.45
1:E:13:GLN:O	1:E:13:GLN:CG	2.64	0.45
1:E:171:LEU:HD13	1:F:129:ILE:CD1	2.45	0.45
1:A:13:GLN:CG	1:A:13:GLN:O	2.65	0.45
1:C:178:TYR:CD2	1:D:189:TYR:HB2	2.52	0.45
1:D:9:SER:H	1:D:231:GLN:HE22	1.64	0.45
1:E:9:SER:H	1:E:231:GLN:HE22	1.65	0.45
1:E:258:LEU:HD22	1:E:272:ASN:HB3	1.98	0.45
1:F:184:PHE:CZ	1:F:232:PHE:HB2	2.52	0.45
1:C:56:ARG:CZ	1:C:328:VAL:HG21	2.47	0.45
1:D:87:GLN:CA	1:D:135:MET:HE2	2.46	0.45
1:C:17:THR:O	1:C:18:ARG:HB3	2.17	0.44
1:C:283:VAL:HG21	1:C:357:ILE:HG13	1.99	0.44
1:D:220:ARG:HG3	1:D:220:ARG:HH11	1.81	0.44
1:F:188:GLU:C	1:F:190:SER:H	2.26	0.44
1:B:87:GLN:HG2	1:B:121:LYS:HZ3	1.82	0.44
1:F:86:PRO:O	1:F:121:LYS:HD3	2.17	0.44
1:B:173:GLU:HG2	1:B:200:SER:OG	2.17	0.44
1:C:198:SER:O	1:C:199:PRO:C	2.60	0.44
1:E:56:ARG:CZ	1:E:328:VAL:HG21	2.47	0.44
1:B:13:GLN:O	1:B:13:GLN:CG	2.64	0.44
1:E:262:VAL:HG23	1:E:313:VAL:HG22	1.99	0.44
1:F:29:VAL:CG1	1:F:230:VAL:CG1	2.90	0.44
1:F:65:LEU:HD22	1:F:69:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:VAL:HG11	1:B:199:PRO:HG2	2.00	0.44
1:B:324:ASP:OD1	1:B:327:GLN:HG2	2.18	0.44
1:D:65:LEU:HD22	1:D:69:LEU:HD11	1.98	0.44
1:D:92:LEU:HD22	1:D:321:PHE:CE1	2.52	0.44
1:E:176:THR:HG22	1:E:239:ILE:HD11	1.98	0.44
1:C:182:GLN:N	1:C:183:PRO:CD	2.81	0.44
1:D:62:GLU:CG	1:D:65:LEU:HB2	2.48	0.44
1:E:193:ILE:HG22	1:E:194:GLY:N	2.31	0.44
1:F:62:GLU:CG	1:F:65:LEU:HB2	2.47	0.44
1:F:16:THR:C	1:F:17:THR:HG22	2.42	0.44
1:F:56:ARG:CZ	1:F:328:VAL:HG21	2.48	0.44
1:A:82:ILE:HD11	1:A:101:ALA:HB2	2.00	0.43
1:A:25:LEU:HD12	1:A:29:VAL:HG23	1.98	0.43
1:F:203:THR:HG22	1:F:232:PHE:CZ	2.52	0.43
1:B:188:GLU:C	1:B:190:SER:H	2.25	0.43
1:C:268:PRO:HA	1:C:272:ASN:HD22	1.82	0.43
1:C:287:ILE:O	1:C:291:ALA:HB3	2.18	0.43
1:D:225:ASP:O	1:D:252:PHE:HA	2.19	0.43
1:F:18:ARG:HH12	1:F:310:ASP:CG	2.26	0.43
1:D:78:THR:OG1	1:D:110:ILE:HD11	2.18	0.43
1:E:220:ARG:HG3	1:E:220:ARG:HH11	1.84	0.43
1:F:16:THR:C	1:F:17:THR:CG2	2.91	0.43
1:B:274:ILE:HD13	1:B:283:VAL:HG13	1.99	0.43
1:F:193:ILE:HG22	1:F:194:GLY:N	2.30	0.43
1:A:16:THR:C	1:A:17:THR:CG2	2.92	0.43
1:A:181:VAL:HG11	1:A:199:PRO:HG2	2.00	0.43
1:B:86:PRO:O	1:B:121:LYS:HD3	2.18	0.43
1:B:172:VAL:HG11	1:B:203:THR:OG1	2.19	0.43
1:D:279:ASN:ND2	1:D:281:LYS:HE3	2.33	0.43
1:F:13:GLN:CG	1:F:13:GLN:O	2.66	0.43
1:F:82:ILE:HD11	1:F:101:ALA:HB2	2.00	0.43
1:C:197:ALA:CA	1:D:193:ILE:HG23	2.33	0.43
1:D:18:ARG:HH12	1:D:310:ASP:CG	2.26	0.43
1:D:309:CYS:HB3	1:D:315:PHE:CD2	2.54	0.43
1:C:324:ASP:OD1	1:C:327:GLN:HG2	2.19	0.43
1:A:62:GLU:CG	1:A:65:LEU:HB2	2.49	0.42
1:E:17:THR:O	1:E:18:ARG:HB3	2.18	0.42
1:D:82:ILE:HD11	1:D:101:ALA:HB2	2.01	0.42
1:C:178:TYR:HD2	1:D:189:TYR:HB2	1.84	0.42
1:D:188:GLU:C	1:D:190:SER:H	2.27	0.42
1:F:92:LEU:HD22	1:F:321:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:LEU:HD23	1:A:13:GLN:NE2	2.34	0.42
1:A:68:PHE:O	1:A:72:VAL:HG23	2.19	0.42
1:A:131:GLU:O	1:A:135:MET:HG3	2.20	0.42
1:A:173:GLU:HG2	1:A:200:SER:OG	2.19	0.42
1:A:203:THR:HG22	1:A:232:PHE:CZ	2.55	0.42
1:E:182:GLN:N	1:E:183:PRO:CD	2.82	0.42
1:F:181:VAL:HG11	1:F:199:PRO:HG2	2.00	0.42
1:E:87:GLN:CA	1:E:135:MET:HE2	2.49	0.42
1:A:65:LEU:HD22	1:A:69:LEU:HD11	1.99	0.42
1:A:283:VAL:HG21	1:A:357:ILE:HG13	2.01	0.42
1:D:166:TYR:O	1:D:167:ARG:C	2.60	0.42
1:D:125:ARG:HH22	1:D:192:ASN:HB3	1.85	0.42
1:F:267:ILE:O	1:F:267:ILE:HG23	2.20	0.42
1:C:188:GLU:C	1:C:190:SER:H	2.28	0.41
1:E:171:LEU:CD1	1:F:129:ILE:CD1	2.98	0.41
1:A:16:THR:C	1:A:17:THR:HG22	2.44	0.41
1:D:268:PRO:HA	1:D:272:ASN:HD22	1.85	0.41
1:E:188:GLU:C	1:E:190:SER:H	2.28	0.41
1:F:305:LEU:HD22	1:F:305:LEU:HA	1.91	0.41
1:A:213:HIS:O	1:C:130:ASN:ND2	2.53	0.41
1:C:225:ASP:O	1:C:252:PHE:HA	2.19	0.41
1:E:283:VAL:HG21	1:E:357:ILE:HG13	2.03	0.41
1:A:184:PHE:CZ	1:A:232:PHE:HB2	2.56	0.41
1:B:324:ASP:O	1:B:328:VAL:HG23	2.19	0.41
1:C:220:ARG:HG3	1:C:220:ARG:HH11	1.84	0.41
1:D:193:ILE:HG22	1:D:194:GLY:N	2.35	0.41
1:E:62:GLU:CG	1:E:65:LEU:HB2	2.51	0.41
1:E:141:LYS:HA	1:E:367:ILE:HG21	2.01	0.41
1:E:309:CYS:HB3	1:E:315:PHE:CD2	2.55	0.41
1:B:62:GLU:CG	1:B:65:LEU:HB2	2.51	0.41
1:C:261:GLY:CA	1:C:262:VAL:HB	2.51	0.41
1:D:367:ILE:N	1:D:367:ILE:HD12	2.34	0.41
1:B:214:PHE:C	1:E:130:ASN:ND2	2.78	0.41
1:E:18:ARG:HH12	1:E:310:ASP:CG	2.28	0.41
1:E:268:PRO:HA	1:E:272:ASN:HD22	1.86	0.41
1:A:80:ILE:HB	1:A:112:VAL:HG22	2.03	0.41
1:C:267:ILE:O	1:C:267:ILE:HG23	2.21	0.41
1:C:309:CYS:HB3	1:C:315:PHE:CD2	2.55	0.41
1:F:118:ASP:N	1:F:118:ASP:OD1	2.53	0.41
1:A:188:GLU:C	1:A:190:SER:H	2.29	0.41
1:B:315:PHE:O	1:B:316:GLN:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:18:ARG:HH12	1:C:310:ASP:CG	2.29	0.41
1:C:64:SER:HB2	1:C:249:THR:CG2	2.50	0.41
1:C:82:ILE:HD11	1:C:101:ALA:HB2	2.03	0.41
1:F:172:VAL:HG11	1:F:203:THR:OG1	2.19	0.41
1:C:11:LEU:C	1:C:13:GLN:N	2.77	0.41
1:C:184:PHE:CZ	1:C:232:PHE:HB2	2.56	0.41
1:D:56:ARG:CZ	1:D:328:VAL:HG21	2.50	0.41
1:E:25:LEU:HD12	1:E:29:VAL:HG23	2.02	0.41
1:F:117:LEU:HD13	1:F:120:ILE:HD12	2.03	0.41
1:F:141:LYS:HA	1:F:367:ILE:HG21	2.02	0.41
1:F:225:ASP:O	1:F:252:PHE:HA	2.21	0.41
1:A:193:ILE:HG21	1:A:193:ILE:HD13	1.68	0.41
1:C:167:ARG:CZ	1:D:159:TYR:HB3	2.51	0.41
1:D:258:LEU:HD22	1:D:272:ASN:CB	2.49	0.41
1:B:225:ASP:O	1:B:252:PHE:HA	2.20	0.40
1:F:279:ASN:ND2	1:F:281:LYS:HE3	2.36	0.40
1:A:141:LYS:HA	1:A:367:ILE:HG21	2.03	0.40
1:A:274:ILE:HD13	1:A:283:VAL:HG13	2.02	0.40
1:B:16:THR:OG1	1:B:20:THR:HA	2.22	0.40
1:C:375:TYR:CD2	1:C:375:TYR:C	2.99	0.40
1:D:86:PRO:O	1:D:121:LYS:HD3	2.20	0.40
1:F:261:GLY:CA	1:F:262:VAL:HB	2.51	0.40
1:D:16:THR:OG1	1:D:20:THR:HA	2.21	0.40
1:D:141:LYS:HA	1:D:367:ILE:HG21	2.03	0.40
1:D:181:VAL:C	1:D:183:PRO:CD	2.94	0.40
1:D:283:VAL:HG21	1:D:357:ILE:HG13	2.02	0.40
1:A:179:ASN:HB3	1:B:189:TYR:CD1	2.57	0.40
1:A:214:PHE:HA	1:C:130:ASN:HD22	1.86	0.40
1:C:29:VAL:CG1	1:C:230:VAL:CG1	2.92	0.40
1:C:222:LEU:HD12	1:C:222:LEU:C	2.46	0.40
1:F:117:LEU:HD22	1:F:120:ILE:HD12	2.03	0.40
1:A:262:VAL:HG23	1:A:313:VAL:HG22	2.03	0.40
1:B:309:CYS:HB3	1:B:315:PHE:CD2	2.56	0.40
1:D:172:VAL:HG11	1:D:203:THR:OG1	2.21	0.40

All (6) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:GLU:OE2	1:C:244:ASN:ND2[2_546]	1.90	0.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:189:TYR:CB	1:C:37:GLN:NE2[1_655]	1.97	0.23
1:A:189:TYR:OH	1:C:43:GLU:OE1[1_655]	2.00	0.20
1:B:355:ASP:OD2	1:F:88:LYS:NZ[2_555]	2.09	0.11
1:A:40:GLN:NE2	1:F:18:ARG:NE[1_556]	2.14	0.06
1:A:355:ASP:OD2	1:D:88:LYS:NZ[2_546]	2.17	0.03

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	372/386 (96%)	345 (93%)	19 (5%)	8 (2%)	5	26
1	B	372/386 (96%)	347 (93%)	16 (4%)	9 (2%)	4	24
1	C	372/386 (96%)	346 (93%)	17 (5%)	9 (2%)	4	24
1	D	372/386 (96%)	347 (93%)	16 (4%)	9 (2%)	4	24
1	E	372/386 (96%)	347 (93%)	16 (4%)	9 (2%)	4	24
1	F	372/386 (96%)	346 (93%)	17 (5%)	9 (2%)	4	24
All	All	2232/2316 (96%)	2078 (93%)	101 (4%)	53 (2%)	4	24

All (53) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	12	LEU
1	A	22	TYR
1	A	182	GLN
1	A	228	LYS
1	A	310	ASP
1	B	12	LEU
1	B	182	GLN
1	B	228	LYS
1	B	310	ASP
1	C	182	GLN

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Mol	Chain	Res	Type
1	C	228	LYS
1	C	262	VAL
1	C	305	LEU
1	C	310	ASP
1	D	12	LEU
1	D	182	GLN
1	D	262	VAL
1	D	310	ASP
1	E	182	GLN
1	E	228	LYS
1	E	310	ASP
1	F	12	LEU
1	F	182	GLN
1	F	262	VAL
1	F	310	ASP
1	A	262	VAL
1	A	305	LEU
1	B	22	TYR
1	B	262	VAL
1	B	305	LEU
1	C	12	LEU
1	C	22	TYR
1	D	22	TYR
1	D	183	PRO
1	D	228	LYS
1	D	266	ASP
1	D	305	LEU
1	E	12	LEU
1	E	22	TYR
1	E	262	VAL
1	E	305	LEU
1	F	22	TYR
1	F	183	PRO
1	F	228	LYS
1	F	305	LEU
1	A	183	PRO
1	B	183	PRO
1	B	266	ASP
1	C	183	PRO
1	E	183	PRO
1	F	266	ASP
1	E	266	ASP

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Mol	Chain	Res	Type
1	C	266	ASP

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	323/348 (93%)	292 (90%)	31 (10%)	8	31
1	B	322/348 (92%)	292 (91%)	30 (9%)	8	32
1	C	323/348 (93%)	295 (91%)	28 (9%)	9	35
1	D	323/348 (93%)	295 (91%)	28 (9%)	9	35
1	E	322/348 (92%)	291 (90%)	31 (10%)	8	31
1	F	323/348 (93%)	292 (90%)	31 (10%)	8	31
All	All	1936/2088 (93%)	1757 (91%)	179 (9%)	8	33

All (179) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LEU
1	A	13	GLN
1	A	17	THR
1	A	20	THR
1	A	39	ILE
1	A	60	LEU
1	A	62	GLU
1	A	65	LEU
1	A	92	LEU
1	A	110	ILE
1	A	168	THR
1	A	171	LEU
1	A	181	VAL
1	A	189	TYR
1	A	193	ILE
1	A	198	SER
1	A	212	SER

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Mol	Chain	Res	Type
1	A	220	ARG
1	A	222	LEU
1	A	227	ILE
1	A	249	THR
1	A	273	SER
1	A	275	LEU
1	A	285	ARG
1	A	298	THR
1	A	311	ILE
1	A	327	GLN
1	A	341	LEU
1	A	342	SER
1	A	369	THR
1	A	379	THR
1	B	11	LEU
1	B	13	GLN
1	B	17	THR
1	B	20	THR
1	B	39	ILE
1	B	62	GLU
1	B	65	LEU
1	B	92	LEU
1	B	110	ILE
1	B	168	THR
1	B	171	LEU
1	B	176	THR
1	B	181	VAL
1	B	189	TYR
1	B	193	ILE
1	B	198	SER
1	B	220	ARG
1	B	222	LEU
1	B	227	ILE
1	B	249	THR
1	B	273	SER
1	B	275	LEU
1	B	285	ARG
1	B	298	THR
1	B	311	ILE
1	B	327	GLN
1	B	341	LEU
1	B	342	SER

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Mol	Chain	Res	Type
1	B	369	THR
1	B	379	THR
1	C	11	LEU
1	C	13	GLN
1	C	17	THR
1	C	20	THR
1	C	39	ILE
1	C	62	GLU
1	C	65	LEU
1	C	92	LEU
1	C	110	ILE
1	C	168	THR
1	C	171	LEU
1	C	181	VAL
1	C	189	TYR
1	C	193	ILE
1	C	198	SER
1	C	220	ARG
1	C	222	LEU
1	C	227	ILE
1	C	249	THR
1	C	273	SER
1	C	275	LEU
1	C	285	ARG
1	C	298	THR
1	C	311	ILE
1	C	327	GLN
1	C	341	LEU
1	C	342	SER
1	C	379	THR
1	D	11	LEU
1	D	13	GLN
1	D	17	THR
1	D	20	THR
1	D	39	ILE
1	D	62	GLU
1	D	65	LEU
1	D	92	LEU
1	D	110	ILE
1	D	168	THR
1	D	171	LEU
1	D	181	VAL

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Mol	Chain	Res	Type
1	D	189	TYR
1	D	193	ILE
1	D	198	SER
1	D	220	ARG
1	D	222	LEU
1	D	227	ILE
1	D	249	THR
1	D	273	SER
1	D	275	LEU
1	D	285	ARG
1	D	298	THR
1	D	311	ILE
1	D	327	GLN
1	D	341	LEU
1	D	342	SER
1	D	379	THR
1	E	11	LEU
1	E	13	GLN
1	E	17	THR
1	E	20	THR
1	E	39	ILE
1	E	60	LEU
1	E	62	GLU
1	E	65	LEU
1	E	92	LEU
1	E	110	ILE
1	E	168	THR
1	E	171	LEU
1	E	176	THR
1	E	181	VAL
1	E	189	TYR
1	E	193	ILE
1	E	198	SER
1	E	220	ARG
1	E	222	LEU
1	E	227	ILE
1	E	249	THR
1	E	273	SER
1	E	275	LEU
1	E	285	ARG
1	E	298	THR
1	E	311	ILE

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Mol	Chain	Res	Type
1	E	327	GLN
1	E	341	LEU
1	E	342	SER
1	E	369	THR
1	E	379	THR
1	F	11	LEU
1	F	13	GLN
1	F	17	THR
1	F	20	THR
1	F	39	ILE
1	F	60	LEU
1	F	62	GLU
1	F	65	LEU
1	F	92	LEU
1	F	110	ILE
1	F	168	THR
1	F	171	LEU
1	F	181	VAL
1	F	189	TYR
1	F	193	ILE
1	F	198	SER
1	F	220	ARG
1	F	222	LEU
1	F	227	ILE
1	F	249	THR
1	F	273	SER
1	F	275	LEU
1	F	285	ARG
1	F	298	THR
1	F	305	LEU
1	F	311	ILE
1	F	324	ASP
1	F	327	GLN
1	F	341	LEU
1	F	342	SER
1	F	379	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	160	GLN
1	A	229	ASN

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Mol	Chain	Res	Type
1	A	272	ASN
1	A	279	ASN
1	A	327	GLN
1	B	272	ASN
1	B	279	ASN
1	C	160	GLN
1	C	229	ASN
1	C	272	ASN
1	C	279	ASN
1	C	327	GLN
1	D	160	GLN
1	D	229	ASN
1	D	272	ASN
1	D	279	ASN
1	D	327	GLN
1	E	160	GLN
1	E	229	ASN
1	E	272	ASN
1	E	279	ASN
1	E	327	GLN
1	F	160	GLN
1	F	229	ASN
1	F	272	ASN
1	F	279	ASN
1	F	327	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

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	374/386 (96%)	-0.26	0 100 100	20, 20, 20, 50	0
1	B	374/386 (96%)	0.05	2 (0%) 87 72	20, 20, 20, 50	0
1	C	374/386 (96%)	0.03	2 (0%) 87 72	20, 20, 20, 50	0
1	D	374/386 (96%)	-0.34	0 100 100	20, 20, 20, 50	0
1	E	374/386 (96%)	-0.07	3 (0%) 82 64	20, 20, 20, 50	0
1	F	374/386 (96%)	-0.51	0 100 100	20, 20, 20, 50	0
All	All	2244/2316 (96%)	-0.18	7 (0%) 90 79	20, 20, 20, 50	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	163	GLY	2.8
1	E	61	ALA	2.7
1	C	193	ILE	2.6
1	B	344	GLU	2.5
1	E	368	THR	2.5
1	E	32	ASN	2.1
1	C	177	ALA	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.