



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:04 AM UTC

PDB ID : 1J5W / pdb_00001j5w
Title : Crystal structure of Glycyl-tRNA synthetase alpha chain (TM0216) from *Thermotoga maritima* at 1.95 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2002-07-05
Resolution : 1.95 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

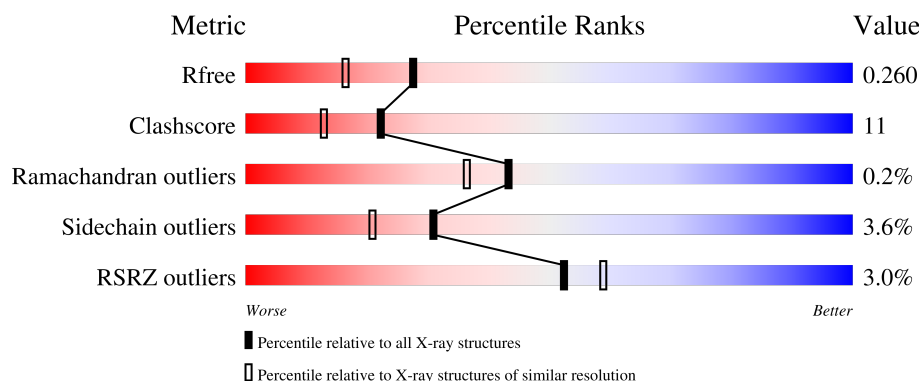
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

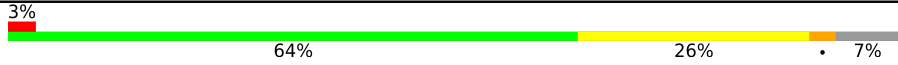
The reported resolution of this entry is 1.95 Å.

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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	298	
1	B	298	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4829 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 Glycyl-tRNA synthetase alpha chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	Se	0	0	0
			2267	1469	373	417	2	6			
1	B	278	Total	C	N	O	S	Se	0	0	0
			2307	1494	382	423	2	6			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MSE	-	expression tag	UNP Q9WY59
A	-10	GLY	-	expression tag	UNP Q9WY59
A	-9	SER	-	expression tag	UNP Q9WY59
A	-8	ASP	-	expression tag	UNP Q9WY59
A	-7	LYS	-	expression tag	UNP Q9WY59
A	-6	ILE	-	expression tag	UNP Q9WY59
A	-5	HIS	-	expression tag	UNP Q9WY59
A	-4	HIS	-	expression tag	UNP Q9WY59
A	-3	HIS	-	expression tag	UNP Q9WY59
A	-2	HIS	-	expression tag	UNP Q9WY59
A	-1	HIS	-	expression tag	UNP Q9WY59
A	0	HIS	-	expression tag	UNP Q9WY59
A	1	MSE	MET	modified residue	UNP Q9WY59
A	8	MSE	MET	modified residue	UNP Q9WY59
A	27	MSE	MET	modified residue	UNP Q9WY59
A	134	MSE	MET	modified residue	UNP Q9WY59
A	166	MSE	MET	modified residue	UNP Q9WY59
A	267	MSE	MET	modified residue	UNP Q9WY59
B	-11	MSE	-	expression tag	UNP Q9WY59
B	-10	GLY	-	expression tag	UNP Q9WY59
B	-9	SER	-	expression tag	UNP Q9WY59
B	-8	ASP	-	expression tag	UNP Q9WY59
B	-7	LYS	-	expression tag	UNP Q9WY59
B	-6	ILE	-	expression tag	UNP Q9WY59
B	-5	HIS	-	expression tag	UNP Q9WY59

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	HIS	-	expression tag	UNP Q9WY59
B	-3	HIS	-	expression tag	UNP Q9WY59
B	-2	HIS	-	expression tag	UNP Q9WY59
B	-1	HIS	-	expression tag	UNP Q9WY59
B	0	HIS	-	expression tag	UNP Q9WY59
B	1	MSE	MET	modified residue	UNP Q9WY59
B	8	MSE	MET	modified residue	UNP Q9WY59
B	27	MSE	MET	modified residue	UNP Q9WY59
B	134	MSE	MET	modified residue	UNP Q9WY59
B	166	MSE	MET	modified residue	UNP Q9WY59
B	267	MSE	MET	modified residue	UNP Q9WY59

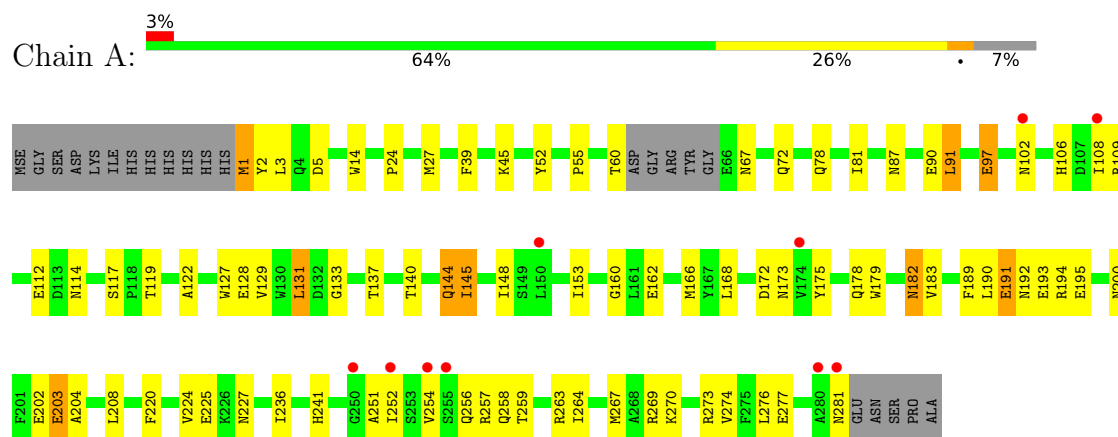
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	115	Total 115	O 115	0	0
2	B	140	Total 140	O 140	0	0

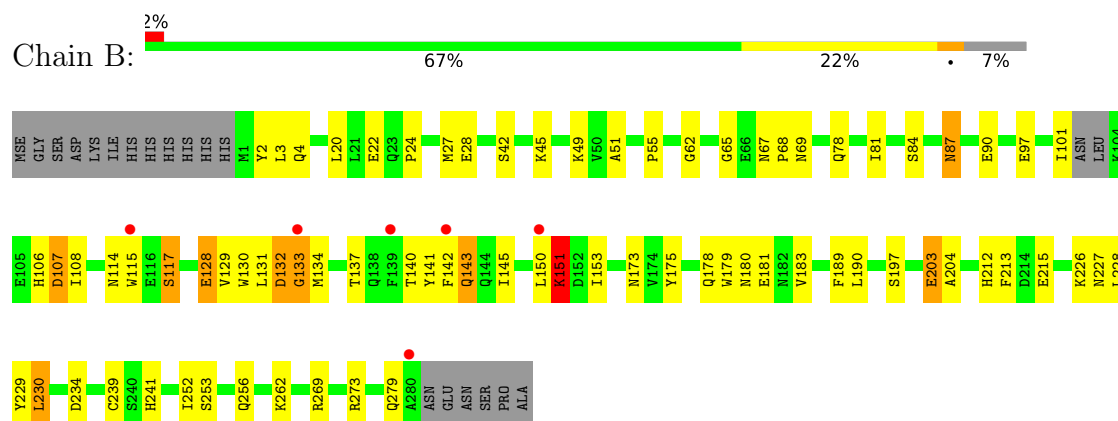
3 Residue-property plots [i](#)

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: Glycyl-tRNA synthetase alpha chain



• Molecule 1: Glycyl-tRNA synthetase alpha chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.40Å 66.20Å 142.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.95 20.00 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.5 (20.00-1.95) 97.3 (20.00-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 1.80Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.197 , 0.254 0.206 , 0.260	Depositor DCC
R_{free} test set	5687 reflections (10.15%)	wwPDB-VP
Wilson B-factor (Å ²)	29.8	Xtriage
Anisotropy	0.431	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4829	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% 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	1.03	8/2324 (0.3%)	1.23	20/3146 (0.6%)
1	B	1.04	8/2365 (0.3%)	1.20	19/3196 (0.6%)
All	All	1.03	16/4689 (0.3%)	1.21	39/6342 (0.6%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	182	ASN	CG-OD1	6.24	1.35	1.23
1	B	241	HIS	ND1-CE1	6.08	1.38	1.32
1	B	279	GLN	CD-OE1	6.04	1.35	1.23
1	A	256	GLN	CD-OE1	5.87	1.34	1.23
1	A	258	GLN	CD-OE1	5.78	1.34	1.23
1	B	4	GLN	CD-OE1	5.68	1.34	1.23
1	B	114	ASN	CG-OD1	5.66	1.34	1.23
1	A	241	HIS	ND1-CE1	5.45	1.38	1.32
1	A	178	GLN	CD-OE1	5.26	1.33	1.23
1	A	144	GLN	CD-NE2	-5.22	1.22	1.33
1	B	256	GLN	CD-OE1	5.14	1.33	1.23
1	B	87	ASN	CG-OD1	5.13	1.33	1.23
1	A	67	ASN	CG-OD1	5.12	1.33	1.23
1	A	241	HIS	CD2-NE2	-5.10	1.32	1.37
1	B	212	HIS	ND1-CE1	5.07	1.37	1.32
1	B	173	ASN	CG-OD1	5.05	1.33	1.23

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	133	GLY	N-CA-C	-10.98	95.04	112.61
1	B	203	GLU	N-CA-C	8.66	124.78	114.04
1	A	117	SER	CA-C-N	8.19	128.66	119.32
1	A	117	SER	C-N-CA	8.19	128.66	119.32
1	A	203	GLU	N-CA-C	8.09	124.33	113.97
1	A	140	THR	N-CA-C	7.84	121.68	108.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	252	ILE	N-CA-C	7.67	119.89	108.46
1	A	258	GLN	N-CA-C	-7.66	102.57	112.23
1	A	200	ASN	N-CA-C	7.64	119.61	111.28
1	B	151	LYS	N-CA-C	-7.62	102.91	111.14
1	A	128	GLU	N-CA-C	-7.61	97.34	109.59
1	B	55	PRO	N-CA-C	-7.32	99.76	111.03
1	B	128	GLU	N-CA-C	-7.01	97.79	109.07
1	B	189	PHE	N-CA-C	6.82	122.70	113.97
1	A	257	ARG	N-CA-C	6.78	120.43	111.75
1	B	212	HIS	CB-CG-CD2	-6.65	122.56	131.20
1	B	97	GLU	N-CA-C	-6.57	104.04	111.07
1	B	117	SER	CA-C-N	6.53	126.03	119.24
1	B	117	SER	C-N-CA	6.53	126.03	119.24
1	B	241	HIS	CB-CG-CD2	-6.53	122.72	131.20
1	A	251	ALA	N-CA-C	6.44	120.75	113.02
1	A	153	ILE	N-CA-C	6.42	113.40	107.56
1	A	122	ALA	N-CA-C	6.34	119.83	109.24
1	A	55	PRO	N-CA-C	-6.18	101.47	110.80
1	A	241	HIS	CB-CG-CD2	-5.94	123.48	131.20
1	B	197	SER	N-CA-C	-5.92	104.91	111.36
1	A	202	GLU	N-CA-C	5.67	120.57	113.43
1	B	212	HIS	CB-CG-ND1	5.60	131.09	122.70
1	B	132	ASP	CB-CA-C	-5.58	104.05	111.63
1	B	241	HIS	CB-CG-ND1	5.57	131.05	122.70
1	A	160	GLY	N-CA-C	-5.44	100.29	113.18
1	A	45	LYS	N-CA-C	-5.42	101.63	110.20
1	B	143	GLN	N-CA-C	-5.40	106.73	113.38
1	B	45	LYS	N-CA-C	-5.31	100.64	109.46
1	B	183	VAL	N-CA-C	5.29	115.89	108.17
1	A	241	HIS	CB-CG-ND1	5.22	130.53	122.70
1	A	183	VAL	N-CA-C	5.17	115.72	108.17
1	B	228	LEU	N-CA-C	-5.16	101.89	109.62
1	A	189	PHE	N-CA-C	5.00	120.22	113.72

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2267	0	2155	46	0
1	B	2307	0	2215	55	0
2	A	115	0	0	6	0
2	B	140	0	0	11	0
All	All	4829	0	4370	95	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 11.

All (95) 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:A:148:ILE:HD13	1:A:276:LEU:HD11	1.48	0.95
1:B:134:MSE:HE3	2:B:419:HOH:O	1.71	0.91
1:B:108:ILE:CD1	1:B:131:LEU:HD13	2.03	0.89
1:A:109:ARG:NH1	2:A:369:HOH:O	2.06	0.87
1:B:108:ILE:HD13	1:B:131:LEU:HD13	1.56	0.86
1:B:142:PHE:CG	1:B:145:ILE:HD11	2.23	0.73
1:A:1:MSE:HE3	1:A:168:LEU:O	1.88	0.73
1:B:134:MSE:HG3	2:B:422:HOH:O	1.90	0.72
1:A:269:ARG:NH2	2:A:323:HOH:O	2.14	0.70
1:B:106:HIS:O	1:B:107:ASP:HB3	1.90	0.69
1:B:134:MSE:HG2	2:B:391:HOH:O	1.94	0.67
1:B:3:LEU:HB3	1:B:179:TRP:HA	1.77	0.66
1:B:90:GLU:HG3	2:B:374:HOH:O	1.94	0.66
1:B:269:ARG:NH1	2:B:375:HOH:O	2.29	0.64
1:B:151:LYS:CD	1:B:151:LYS:H	2.09	0.64
1:A:190:LEU:HD21	1:A:194:ARG:NH1	2.14	0.63
1:A:273:ARG:O	1:A:277:GLU:HG3	1.99	0.63
1:B:273:ARG:HD2	2:B:399:HOH:O	1.99	0.63
1:B:150:LEU:HD22	2:B:423:HOH:O	1.99	0.61
1:B:142:PHE:CD1	1:B:145:ILE:HD11	2.34	0.61
1:A:148:ILE:HD13	1:A:276:LEU:CD1	2.28	0.60
1:A:108:ILE:HG12	1:A:131:LEU:HD23	1.84	0.60
1:B:2:TYR:HE2	1:B:178:GLN:HG2	1.67	0.59
1:B:131:LEU:O	1:B:132:ASP:HB2	2.03	0.58
1:A:191:GLU:OE1	1:A:195:GLU:OE1	2.21	0.58
1:A:208:LEU:HD11	1:B:215:GLU:HB3	1.85	0.57
1:A:24:PRO:HG2	1:B:24:PRO:HD2	1.85	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:ILE:HD13	1:B:131:LEU:CD1	2.31	0.56
1:A:87:ASN:HB3	1:A:90:GLU:OE2	2.05	0.56
1:A:224:VAL:HG22	1:A:274:VAL:HG21	1.88	0.56
1:A:27:MSE:HE2	1:B:28:GLU:CD	2.31	0.56
1:A:259:THR:O	1:A:263:ARG:HG3	2.06	0.56
1:A:162:GLU:O	1:A:166:MSE:HG3	2.06	0.55
1:B:115:TRP:CZ2	1:B:117:SER:HB2	2.41	0.55
1:B:181:GLU:HG3	2:B:355:HOH:O	2.07	0.55
1:A:114:ASN:HB2	2:A:367:HOH:O	2.06	0.55
1:B:133:GLY:O	1:B:134:MSE:HB2	2.07	0.54
1:A:173:ASN:HD21	1:A:175:TYR:HD1	1.56	0.54
1:A:264:ILE:HA	1:A:267:MSE:HE3	1.90	0.54
1:B:84:SER:HG	1:B:141:TYR:HE2	1.54	0.54
1:A:119:THR:HB	1:A:264:ILE:HG21	1.90	0.53
1:B:49:LYS:HD2	2:B:393:HOH:O	2.08	0.53
1:B:151:LYS:H	1:B:151:LYS:HE2	1.73	0.52
1:A:2:TYR:HB2	1:A:5:ASP:OD2	2.10	0.52
1:A:227:ASN:OD1	2:A:362:HOH:O	2.19	0.51
1:B:108:ILE:HD11	1:B:131:LEU:HD13	1.91	0.50
1:A:119:THR:HB	1:A:264:ILE:CG2	2.41	0.50
1:A:102:ASN:O	1:A:106:HIS:HD2	1.93	0.50
1:B:262:LYS:NZ	2:B:426:HOH:O	2.44	0.49
1:A:203:GLU:O	1:A:204:ALA:C	2.55	0.49
1:A:148:ILE:CD1	1:A:276:LEU:HD11	2.33	0.49
1:A:14:TRP:CZ3	1:A:81:ILE:HD11	2.48	0.49
1:B:229:TYR:CE1	1:B:230:LEU:HD13	2.48	0.49
1:B:226:LYS:O	1:B:227:ASN:HB2	2.13	0.49
1:A:179:TRP:CD2	1:B:20:LEU:HD11	2.48	0.48
1:B:132:ASP:C	1:B:133:GLY:O	2.52	0.48
1:B:151:LYS:H	1:B:151:LYS:CE	2.26	0.48
1:A:173:ASN:OD1	1:A:175:TYR:HB2	2.12	0.48
1:B:213:PHE:CE1	1:B:239:CYS:HB3	2.49	0.48
1:B:252:ILE:HG22	1:B:253:SER:O	2.13	0.48
1:B:106:HIS:O	1:B:107:ASP:CB	2.58	0.48
1:B:178:GLN:HG3	1:B:180:ASN:O	2.13	0.48
1:B:49:LYS:HG2	1:B:81:ILE:HG23	1.97	0.47
1:A:39:PHE:CD1	1:A:145:ILE:HD11	2.50	0.47
1:B:115:TRP:CZ3	1:B:142:PHE:CE2	3.04	0.46
1:B:128:GLU:OE2	1:B:130:TRP:NE1	2.46	0.46
1:A:192:ASN:HA	1:B:230:LEU:HD23	1.96	0.46
1:B:129:VAL:HB	1:B:137:THR:HB	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:67:ASN:OD1	1:B:68:PRO:HD2	2.15	0.46
1:B:115:TRP:CE3	1:B:140:THR:HG21	2.51	0.45
1:A:52:TYR:CZ	1:A:78:GLN:HG2	2.51	0.45
1:A:72:GLN:HG3	1:A:193:GLU:OE2	2.17	0.45
1:A:190:LEU:HD21	1:A:194:ARG:HH12	1.81	0.44
1:A:220:PHE:CE1	1:A:236:ILE:HD11	2.53	0.44
1:A:129:VAL:HB	1:A:137:THR:HB	2.00	0.44
1:A:112:GLU:HA	1:A:127:TRP:CD1	2.53	0.43
1:B:62:GLY:HA3	2:B:325:HOH:O	2.17	0.43
1:B:27:MSE:HE1	1:B:234:ASP:OD2	2.18	0.43
1:B:87:ASN:OD1	1:B:87:ASN:N	2.35	0.43
1:A:281:ASN:OD1	1:A:281:ASN:N	2.51	0.43
1:B:42:SER:O	1:B:150:LEU:HD11	2.18	0.43
1:B:101:ILE:HG22	1:B:101:ILE:O	2.17	0.43
1:A:270:LYS:O	1:A:274:VAL:HG23	2.18	0.43
1:B:203:GLU:O	1:B:204:ALA:C	2.59	0.43
1:A:254:VAL:CG2	2:A:400:HOH:O	2.67	0.42
1:B:65:GLY:HA2	1:B:175:TYR:OH	2.19	0.42
1:A:144:GLN:HA	1:A:148:ILE:O	2.19	0.42
1:B:51:ALA:HA	1:B:78:GLN:O	2.21	0.41
1:A:148:ILE:CD1	1:A:276:LEU:CD1	2.98	0.41
1:A:133:GLY:HA2	2:A:369:HOH:O	2.20	0.41
1:A:97:GLU:OE2	1:A:102:ASN:HA	2.21	0.40
1:A:24:PRO:HD2	1:B:24:PRO:HG2	2.02	0.40
1:A:91:LEU:HD23	1:A:91:LEU:HA	1.78	0.40
1:B:84:SER:OG	1:B:141:TYR:HE2	2.03	0.40
1:B:142:PHE:O	1:B:153:ILE:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	272/298 (91%)	267 (98%)	5 (2%)	0	100	100
1	B	274/298 (92%)	268 (98%)	5 (2%)	1 (0%)	30	21
All	All	546/596 (92%)	535 (98%)	10 (2%)	1 (0%)	43	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	107	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	236/255 (92%)	225 (95%)	11 (5%)	23	12
1	B	242/255 (95%)	236 (98%)	6 (2%)	42	34
All	All	478/510 (94%)	461 (96%)	17 (4%)	31	21

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MSE
1	A	3	LEU
1	A	60	THR
1	A	91	LEU
1	A	97	GLU
1	A	131	LEU
1	A	145	ILE
1	A	172	ASP
1	A	182	ASN
1	A	191	GLU
1	A	225	GLU
1	B	22	GLU
1	B	69	ASN
1	B	143	GLN
1	B	151	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	190	LEU
1	B	230	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	143	GLN
1	A	200	ASN
1	B	69	ASN
1	B	173	ASN
1	B	200	ASN

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 [i](#)

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	270/298 (90%)	0.18	10 (3%) 45 52	18, 33, 50, 66	0
1	B	272/298 (91%)	0.06	6 (2%) 62 69	17, 30, 50, 60	0
All	All	542/596 (90%)	0.12	16 (2%) 52 59	17, 32, 50, 66	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	115	TRP	4.8
1	B	133	GLY	4.1
1	B	150	LEU	3.7
1	A	280	ALA	3.3
1	A	150	LEU	2.7
1	A	255	SER	2.5
1	B	280	ALA	2.5
1	A	281	ASN	2.4
1	A	254	VAL	2.4
1	A	250	GLY	2.3
1	A	252	ILE	2.3
1	A	102	ASN	2.2
1	A	174	VAL	2.2
1	A	108	ILE	2.1
1	B	139	PHE	2.1
1	B	142	PHE	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.