



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:32 PM UTC

PDB ID : 9O66 / pdb_00009o66
Title : Crystal Structure of Tryptophanyl-tRNA synthetase from *Klebsiella aerogenes*
Authors : Seattle Structural Genomics Center for Infectious Disease; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2025-04-11
Resolution : 2.10 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

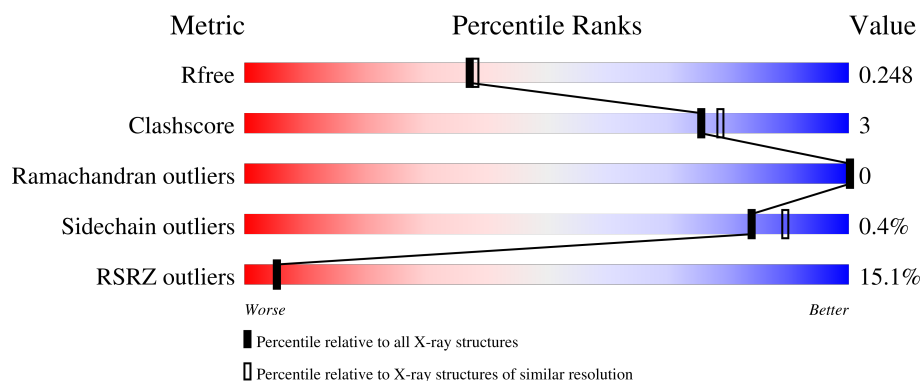
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	355	12% 83% 6% 11%
1	B	355	14% 82% 6% 12%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5009 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 Tryptophan-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	2	0
			2458	1556	422	467	13			
1	B	314	Total	C	N	O	S	0	1	0
			2371	1505	402	451	13			

There are 42 discrepancies between the modelled and reference sequences:

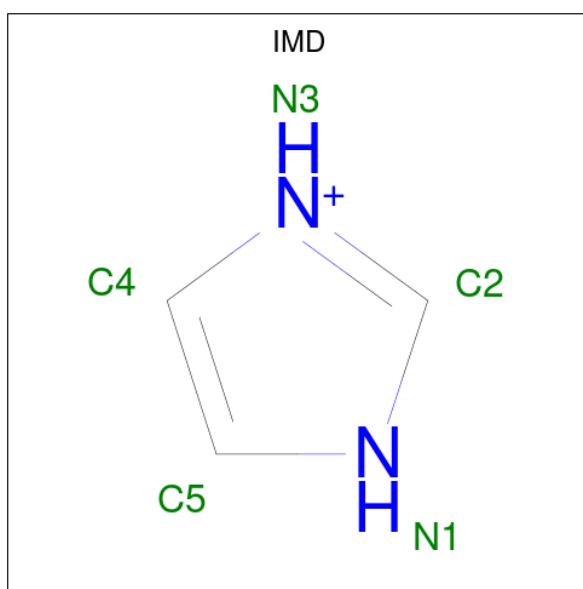
Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP A0A0H3FKK2
A	-19	ALA	-	expression tag	UNP A0A0H3FKK2
A	-18	HIS	-	expression tag	UNP A0A0H3FKK2
A	-17	HIS	-	expression tag	UNP A0A0H3FKK2
A	-16	HIS	-	expression tag	UNP A0A0H3FKK2
A	-15	HIS	-	expression tag	UNP A0A0H3FKK2
A	-14	HIS	-	expression tag	UNP A0A0H3FKK2
A	-13	HIS	-	expression tag	UNP A0A0H3FKK2
A	-12	MET	-	expression tag	UNP A0A0H3FKK2
A	-11	GLY	-	expression tag	UNP A0A0H3FKK2
A	-10	THR	-	expression tag	UNP A0A0H3FKK2
A	-9	LEU	-	expression tag	UNP A0A0H3FKK2
A	-8	GLU	-	expression tag	UNP A0A0H3FKK2
A	-7	ALA	-	expression tag	UNP A0A0H3FKK2
A	-6	GLN	-	expression tag	UNP A0A0H3FKK2
A	-5	THR	-	expression tag	UNP A0A0H3FKK2
A	-4	GLN	-	expression tag	UNP A0A0H3FKK2
A	-3	GLY	-	expression tag	UNP A0A0H3FKK2
A	-2	PRO	-	expression tag	UNP A0A0H3FKK2
A	-1	GLY	-	expression tag	UNP A0A0H3FKK2
A	0	SER	-	expression tag	UNP A0A0H3FKK2
B	-20	MET	-	initiating methionine	UNP A0A0H3FKK2
B	-19	ALA	-	expression tag	UNP A0A0H3FKK2
B	-18	HIS	-	expression tag	UNP A0A0H3FKK2
B	-17	HIS	-	expression tag	UNP A0A0H3FKK2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	HIS	-	expression tag	UNP A0A0H3FKK2
B	-15	HIS	-	expression tag	UNP A0A0H3FKK2
B	-14	HIS	-	expression tag	UNP A0A0H3FKK2
B	-13	HIS	-	expression tag	UNP A0A0H3FKK2
B	-12	MET	-	expression tag	UNP A0A0H3FKK2
B	-11	GLY	-	expression tag	UNP A0A0H3FKK2
B	-10	THR	-	expression tag	UNP A0A0H3FKK2
B	-9	LEU	-	expression tag	UNP A0A0H3FKK2
B	-8	GLU	-	expression tag	UNP A0A0H3FKK2
B	-7	ALA	-	expression tag	UNP A0A0H3FKK2
B	-6	GLN	-	expression tag	UNP A0A0H3FKK2
B	-5	THR	-	expression tag	UNP A0A0H3FKK2
B	-4	GLN	-	expression tag	UNP A0A0H3FKK2
B	-3	GLY	-	expression tag	UNP A0A0H3FKK2
B	-2	PRO	-	expression tag	UNP A0A0H3FKK2
B	-1	GLY	-	expression tag	UNP A0A0H3FKK2
B	0	SER	-	expression tag	UNP A0A0H3FKK2

- Molecule 2 is IMIDAZOLE (CCD ID: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			5	3	2		
2	B	1	Total	C	N	0	0
			5	3	2		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Ca 1	0	0

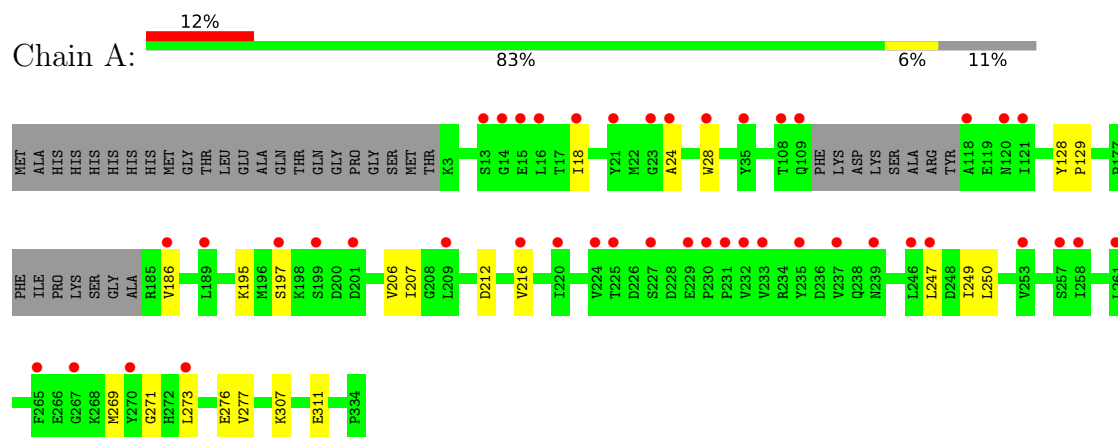
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	80	Total 80	O 80	0	0
4	B	89	Total 89	O 89	0	0

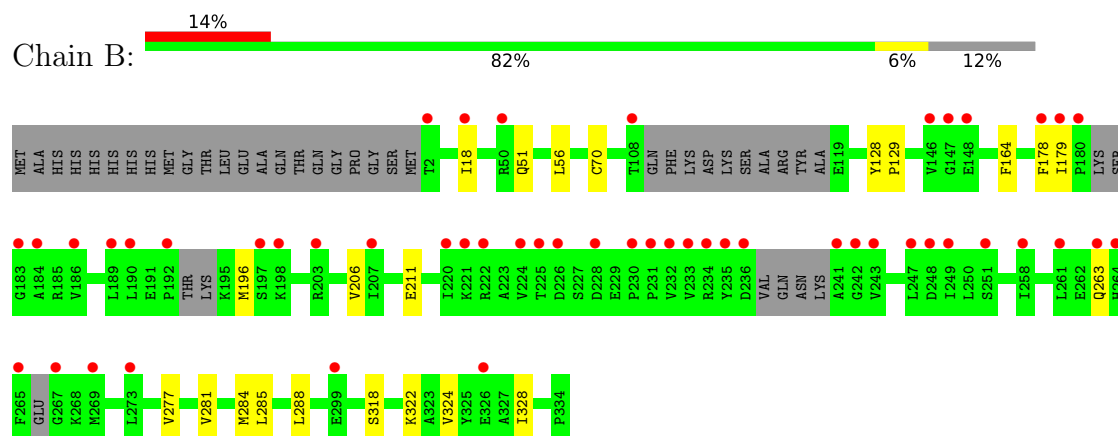
3 Residue-property plots

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: Tryptophan-tRNA ligase



• Molecule 1: Tryptophan-tRNA ligase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	153.16Å 75.51Å 56.75Å 90.00° 95.93° 90.00°	Depositor
Resolution (Å)	43.27 – 2.10 43.27 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (43.27-2.10) 99.7 (43.27-2.10)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 2.10Å)	Xtriage
Refinement program	PHENIX dev_5660	Depositor
R, R_{free}	0.201 , 0.247 0.206 , 0.248	Depositor DCC
R_{free} test set	1840 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.386	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 50.8	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	0.94	EDS
Total number of atoms	5009	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.13% 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

Bond lengths and bond angles in the following residue types are not validated in this section: CA, IMD

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	0.12	0/2514	0.28	0/3411
1	B	0.14	0/2419	0.31	0/3283
All	All	0.13	0/4933	0.30	0/6694

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

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	2458	0	2382	15	0
1	B	2371	0	2264	13	0
2	A	5	0	5	0	0
2	B	5	0	5	0	0
3	B	1	0	0	0	0
4	A	80	0	0	0	0
4	B	89	0	0	0	0
All	All	5009	0	4656	28	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 3.

All (28) 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:18:ILE:HD11	1:A:186:VAL:HG11	1.57	0.86
1:A:186:VAL:HG22	1:A:249:ILE:HG12	1.57	0.86
1:A:18:ILE:CD1	1:A:186:VAL:HG11	2.24	0.67
1:A:307:LYS:O	1:A:311:GLU:HG3	1.95	0.65
1:B:18:ILE:CD1	1:B:285:LEU:HD21	2.30	0.61
1:A:269:MET:HE3	1:A:271:GLY:HA3	1.83	0.61
1:A:195:LYS:HZ2	1:A:197:SER:HA	1.73	0.54
1:B:196:MET:HE2	1:B:206:VAL:HA	1.89	0.54
1:A:24:ALA:HB1	1:A:28[A]:TRP:CZ2	2.43	0.53
1:A:250:LEU:HD21	1:A:276:GLU:HG2	1.91	0.51
1:B:164:PHE:CE2	1:B:328:ILE:HD11	2.47	0.50
1:A:212:ASP:O	1:A:216:VAL:HG23	2.15	0.47
1:B:277:VAL:O	1:B:281:VAL:HG22	2.15	0.46
1:B:318:SER:O	1:B:322:LYS:HE2	2.15	0.46
1:A:195:LYS:HD2	1:A:195:LYS:C	2.41	0.45
1:A:195:LYS:NZ	1:A:197:SER:HA	2.31	0.45
1:A:250:LEU:HD13	1:A:277:VAL:HA	1.98	0.45
1:A:128:TYR:N	1:A:129:PRO:CD	2.81	0.43
1:A:206:VAL:O	1:A:207:ILE:HD13	2.19	0.43
1:B:70:CYS:HA	1:B:288:LEU:HD21	2.01	0.43
1:B:18:ILE:HD11	1:B:284:MET:CE	2.49	0.43
1:B:51:GLN:HG2	1:B:56:LEU:HB2	2.00	0.42
1:A:247:LEU:CD2	1:A:273:LEU:HD21	2.49	0.42
1:B:324:VAL:O	1:B:328:ILE:HD13	2.20	0.42
1:B:178:PHE:CE1	1:B:179:ILE:O	2.72	0.42
1:B:284:MET:HE2	1:B:284:MET:HB3	1.94	0.41
1:B:196:MET:HG3	1:B:206:VAL:HG12	2.01	0.41
1:B:128:TYR:N	1:B:129:PRO:CD	2.84	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	313/355 (88%)	304 (97%)	9 (3%)	0	100	100
1	B	303/355 (85%)	299 (99%)	4 (1%)	0	100	100
All	All	616/710 (87%)	603 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	259/301 (86%)	259 (100%)	0	100	100
1	B	243/301 (81%)	241 (99%)	2 (1%)	73	81
All	All	502/602 (83%)	500 (100%)	2 (0%)	84	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	211	GLU
1	B	263	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	B	11	GLN
1	B	90	GLN
1	B	204	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](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	IMD	A	401	-	5,5,5	0.31	0	5,5,5	0.82	0
2	IMD	B	402	-	5,5,5	0.30	0	5,5,5	0.83	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	IMD	A	401	-	-	-	0/1/1/1
2	IMD	B	402	-	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	317/355 (89%)	0.79	44 (13%) 6 6	16, 41, 89, 116	2 (0%)
1	B	314/355 (88%)	0.83	51 (16%) 4 4	17, 38, 94, 114	1 (0%)
All	All	631/710 (88%)	0.81	95 (15%) 5 5	16, 40, 93, 116	3 (0%)

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	261	LEU	5.1
1	A	14	GLY	5.1
1	B	267	GLY	4.8
1	A	28[A]	TRP	4.8
1	A	186	VAL	4.7
1	B	241	ALA	4.7
1	B	233	VAL	4.5
1	B	235	TYR	4.5
1	B	265	PHE	4.3
1	A	13	SER	4.3
1	B	179	ILE	4.2
1	B	232	VAL	4.1
1	A	231	PRO	4.0
1	B	243	VAL	4.0
1	A	24	ALA	3.9
1	A	118	ALA	3.9
1	B	247	LEU	3.9
1	B	299	GLU	3.7
1	B	225	THR	3.7
1	B	147	GLY	3.7
1	A	16	LEU	3.4
1	A	237	VAL	3.3
1	B	146	VAL	3.3
1	A	261	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	201	ASP	3.2
1	A	18	ILE	3.2
1	A	233	VAL	3.1
1	B	180	PRO	3.1
1	B	178	PHE	3.1
1	B	269	MET	3.0
1	B	226	ASP	3.0
1	A	253	VAL	2.9
1	B	18	ILE	2.9
1	B	236	ASP	2.9
1	B	230	PRO	2.9
1	A	232	VAL	2.9
1	B	258	ILE	2.9
1	A	270	TYR	2.9
1	B	222	ARG	2.8
1	A	23	GLY	2.8
1	A	199	SER	2.7
1	B	189	LEU	2.7
1	A	247	LEU	2.7
1	B	190	LEU	2.7
1	A	265	PHE	2.6
1	B	2	THR	2.6
1	A	225	THR	2.6
1	B	228	ASP	2.6
1	B	184	ALA	2.6
1	B	234	ARG	2.6
1	B	186	VAL	2.6
1	B	242	GLY	2.6
1	B	326	GLU	2.5
1	B	198	LYS	2.5
1	A	273	LEU	2.5
1	A	229	GLU	2.5
1	B	224	VAL	2.5
1	B	108	THR	2.5
1	B	273	LEU	2.5
1	B	264	HIS	2.5
1	B	148	GLU	2.4
1	B	248	ASP	2.4
1	B	220	ILE	2.4
1	B	197	SER	2.4
1	B	50	ARG	2.4
1	A	227	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	263	GLN	2.3
1	B	207	ILE	2.3
1	A	235	TYR	2.3
1	A	120	ASN	2.3
1	A	267	GLY	2.3
1	A	220	ILE	2.3
1	B	251	SER	2.3
1	B	231	PRO	2.3
1	B	249	ILE	2.2
1	A	239	ASN	2.2
1	A	230	PRO	2.2
1	B	203	ARG	2.2
1	B	192	PRO	2.2
1	A	189	LEU	2.2
1	A	246	LEU	2.2
1	A	108	THR	2.2
1	A	209	LEU	2.1
1	A	121	ILE	2.1
1	A	15	GLU	2.1
1	A	35	TYR	2.1
1	A	109	GLN	2.1
1	A	216	VAL	2.1
1	A	257	SER	2.1
1	A	258	ILE	2.0
1	A	224	VAL	2.0
1	A	197	SER	2.0
1	B	221	LYS	2.0
1	B	183	GLY	2.0
1	A	21	TYR	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	IMD	B	402	5/5	0.76	0.15	44,45,52,58	0
2	IMD	A	401	5/5	0.91	0.15	30,31,35,38	0
3	CA	B	401	1/1	1.00	0.04	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.