



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 01:43 AM GMT

PDB ID : 3H0L
Title : Structure of trna-dependent amidotransferase gatcab from aquifex aeolicus
Authors : Wu, J.; Bu, W.; Sheppard, K.; Kitabatake, M.; Soll, D.; Smith, J.L.
Deposited on : 2009-04-09
Resolution : 2.30 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

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

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

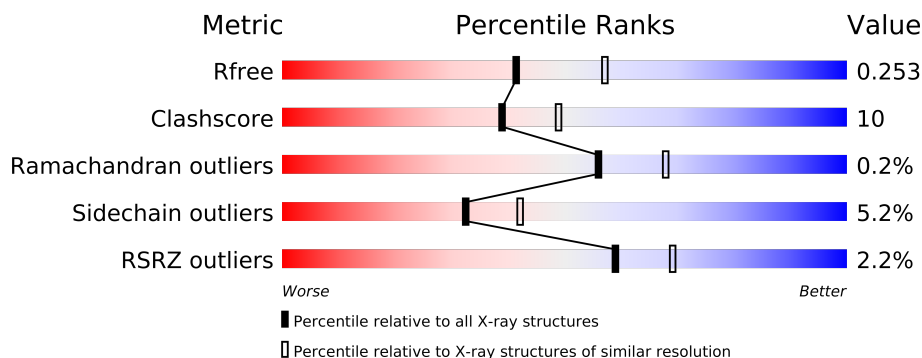
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.30 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.












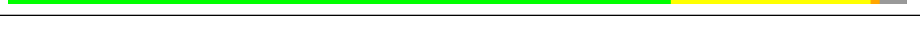
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	478	
1	D	478	
1	G	478	
1	J	478	
1	M	478	
1	P	478	
1	S	478	
1	V	478	
2	B	478	
2	E	478	
2	H	478	
2	K	478	
2	N	478	
2	Q	478	

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Mol	Chain	Length	Quality of chain
2	T	478	
2	W	478	
3	C	94	
3	F	94	
3	I	94	
3	L	94	
3	O	94	
3	R	94	
3	U	94	
3	X	94	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
5	MG	B	801	-	X
5	MG	H	803	-	X
5	MG	N	805	-	X
5	MG	Q	806	-	X
5	MG	T	807	-	X
5	MG	W	808	-	X
7	ASN	M	905	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 63144 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Glutamyl-tRNA(Gln) amidotransferase subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	D	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	G	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	J	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	M	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	P	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	S	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	V	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			

- Molecule 2 is a protein called Aspartyl/glutamyl-tRNA(Asn/Gln)amidotransferase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	E	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	H	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	K	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	N	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	Q	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			

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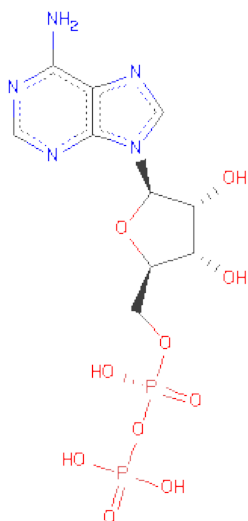
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	W	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			

- Molecule 3 is a protein called Glutamyl-tRNA(Gln) amidotransferase subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	F	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	I	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	L	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	O	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	R	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	U	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	X	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	K	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	N	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	Q	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	T	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	W	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	Q	1	Total	Mg	0	0
			1	1		
5	K	1	Total	Mg	0	0
			1	1		
5	E	1	Total	Mg	0	0
			1	1		
5	H	1	Total	Mg	0	0
			1	1		
5	B	1	Total	Mg	0	0
			1	1		
5	W	1	Total	Mg	0	0
			1	1		
5	T	1	Total	Mg	0	0
			1	1		
5	N	1	Total	Mg	0	0
			1	1		

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

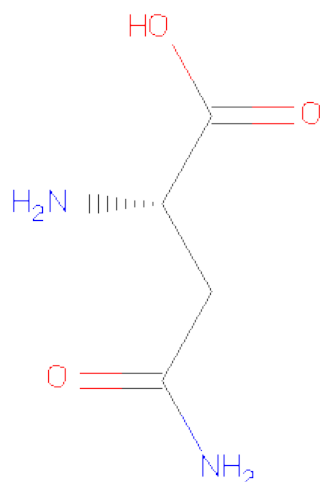
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	Q	1	Total	Zn	0	0
			1	1		
6	K	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	1	Total	Zn	0	0
			1	1		
6	H	1	Total	Zn	0	0
			1	1		
6	B	1	Total	Zn	0	0
			1	1		
6	W	1	Total	Zn	0	0
			1	1		
6	T	1	Total	Zn	0	0
			1	1		
6	N	1	Total	Zn	0	0
			1	1		

- Molecule 7 is ASPARAGINE (three-letter code: ASN) (formula: $C_4H_8N_2O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			8	4	1	3		
7	D	1	Total	C	N	O	0	0
			8	4	1	3		
7	G	1	Total	C	N	O	0	0
			8	4	1	3		
7	J	1	Total	C	N	O	0	0
			8	4	1	3		
7	M	1	Total	C	N	O	0	0
			8	4	1	3		

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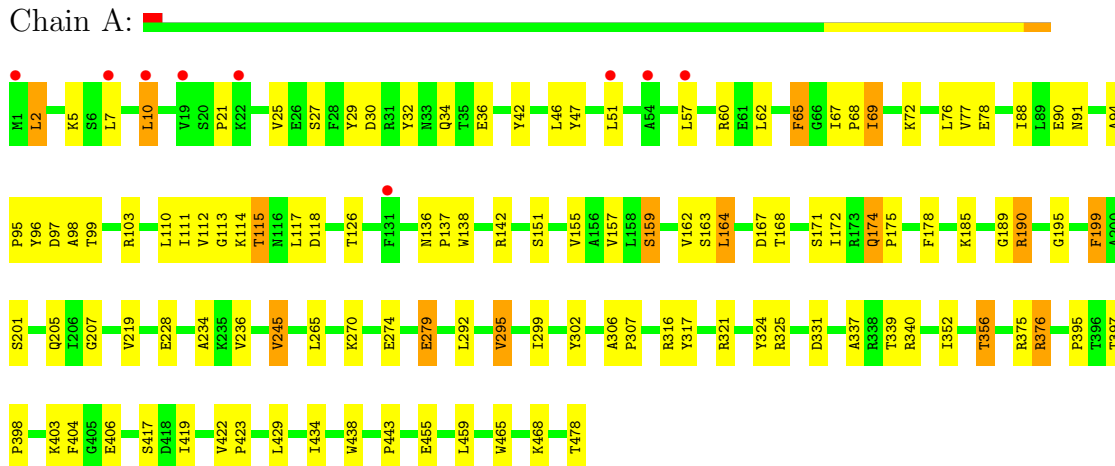
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	P	1	Total	C	N	O	0	0
			8	4	1	3		
7	S	1	Total	C	N	O	0	0
			8	4	1	3		
7	V	1	Total	C	N	O	0	0
			8	4	1	3		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

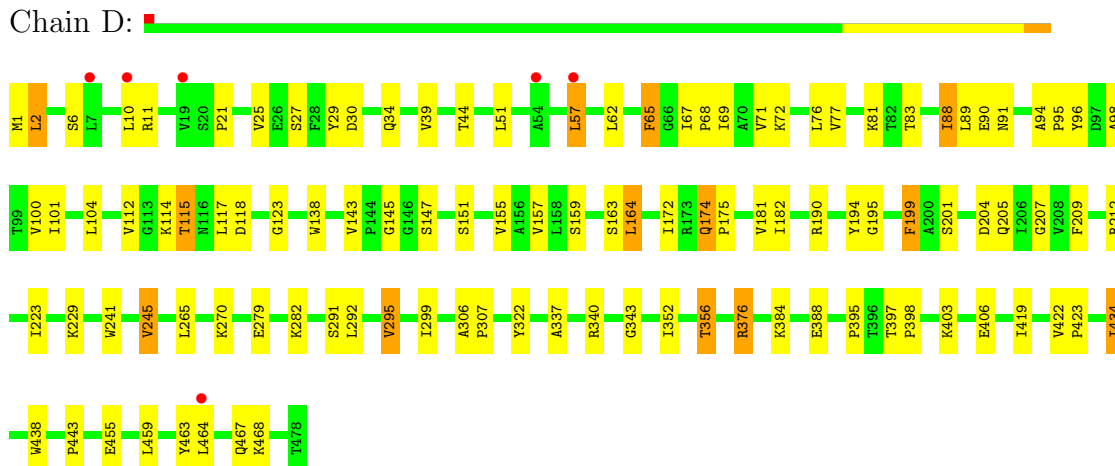
- Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain A:



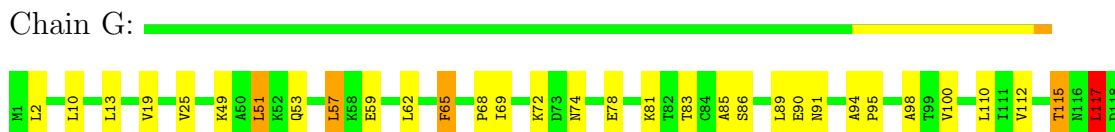
- Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

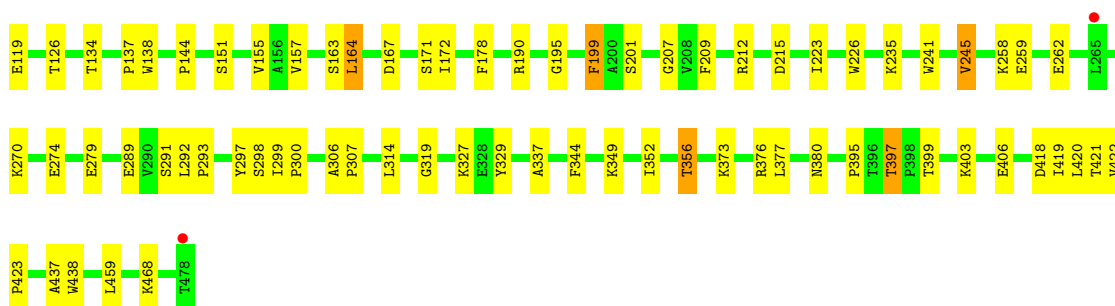
Chain D:



- Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

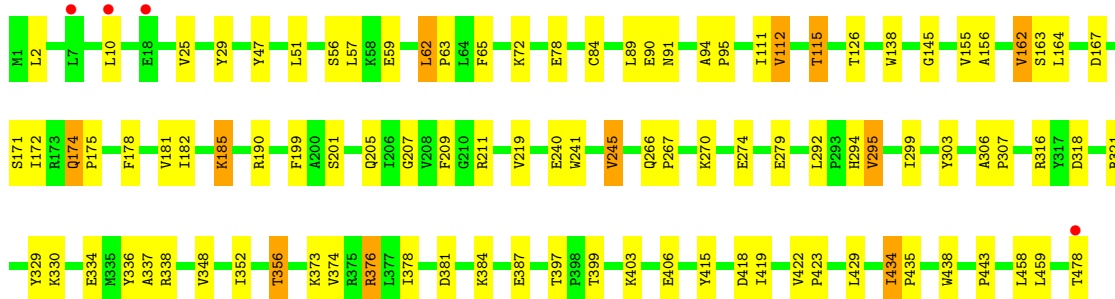
Chain G:





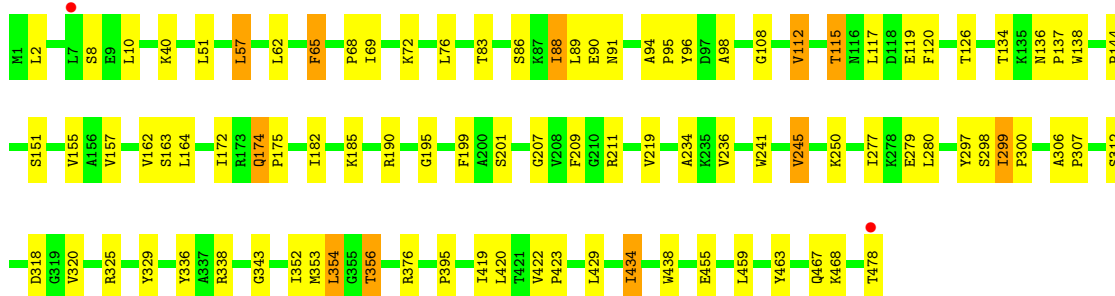
• Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain J:



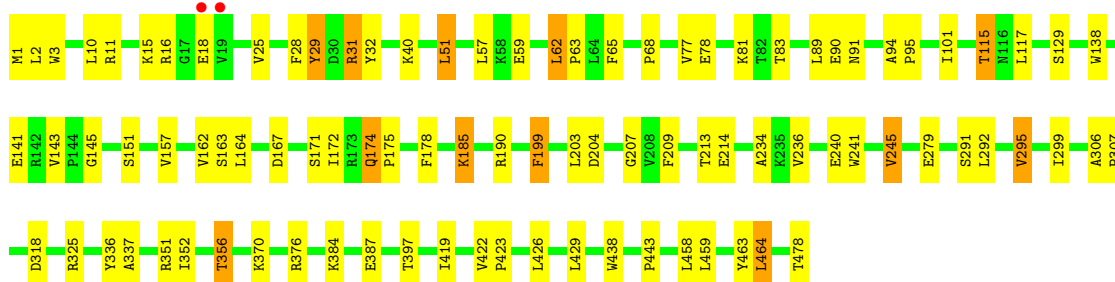
• Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain M:



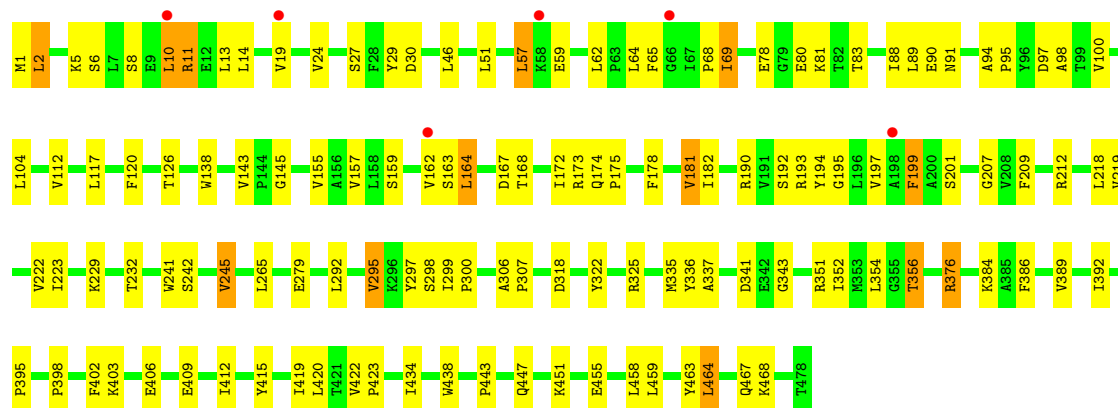
• Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain P:



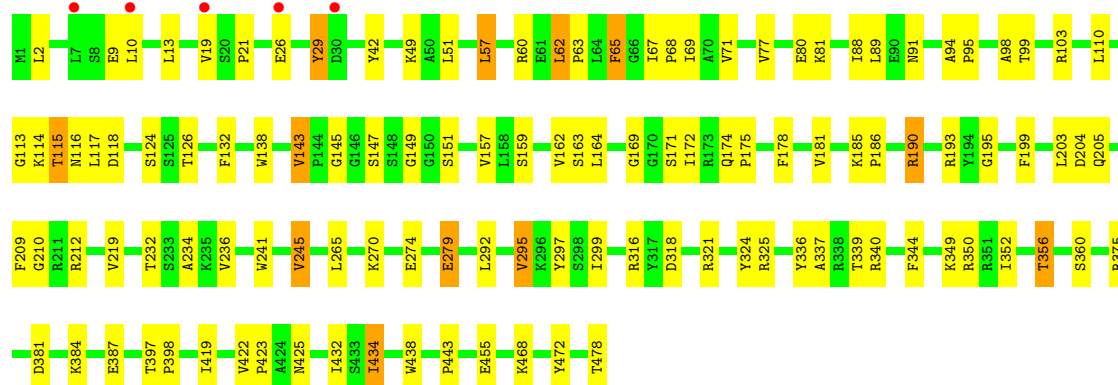
• Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain S:



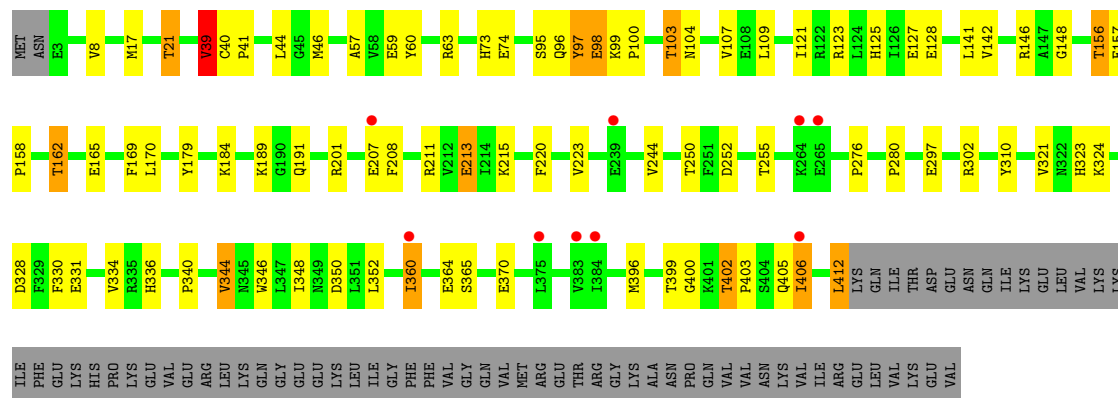
• Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain V:



• Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln)amidotransferase subunit B

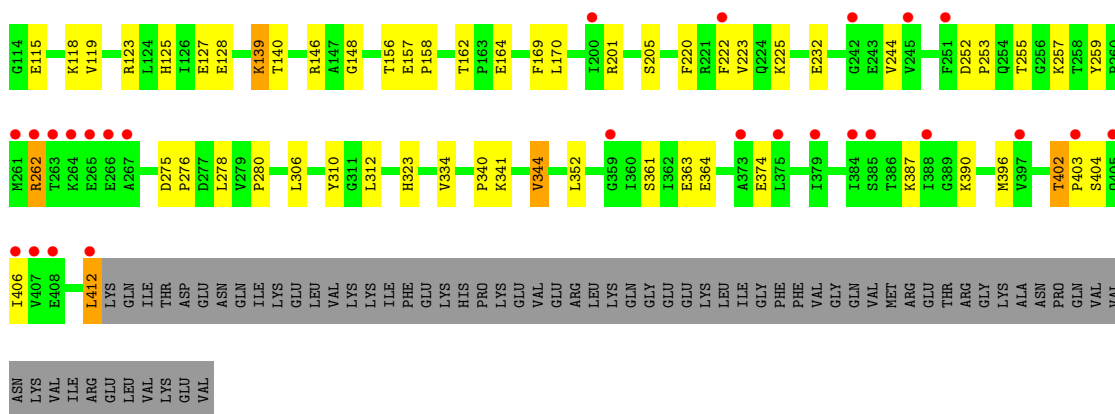
Chain B:



• Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln)amidotransferase subunit B

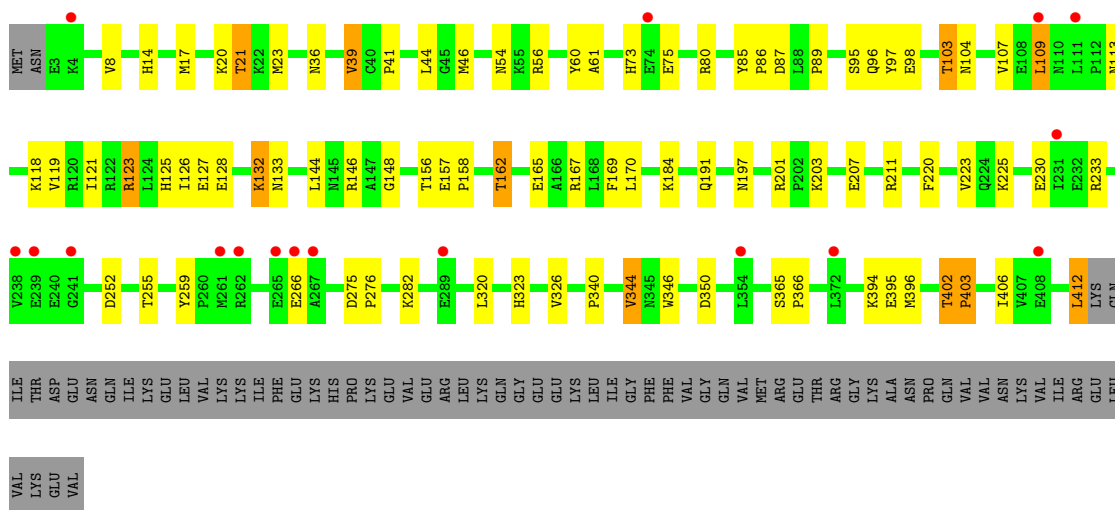
Chain E:





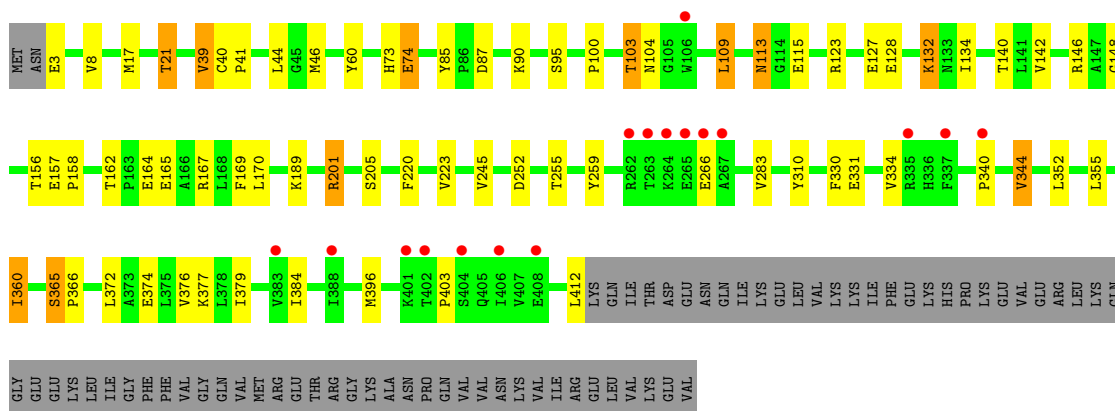
- Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln)amidotransferase subunit B

Chain H:



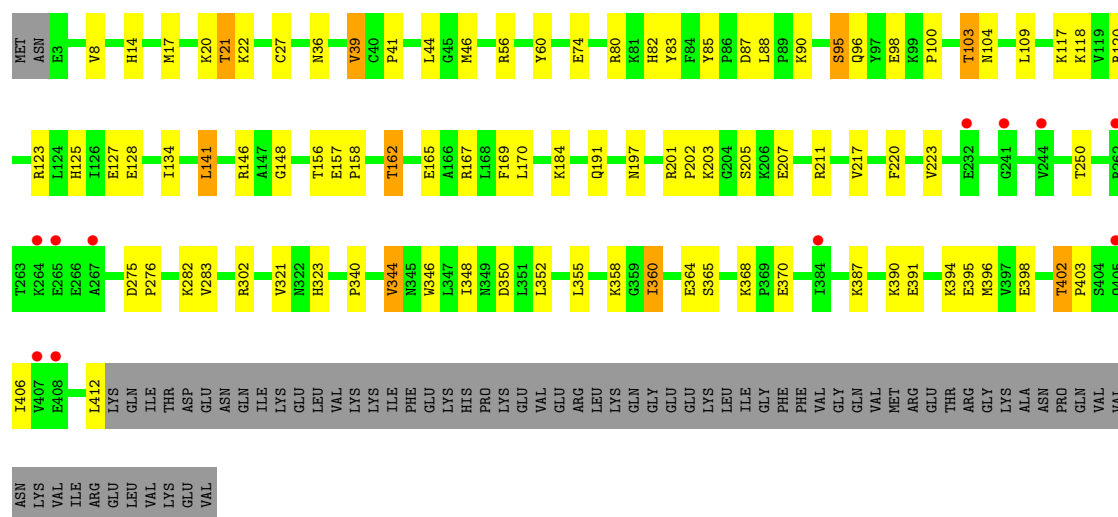
- Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln)amidotransferase subunit B

Chain K:



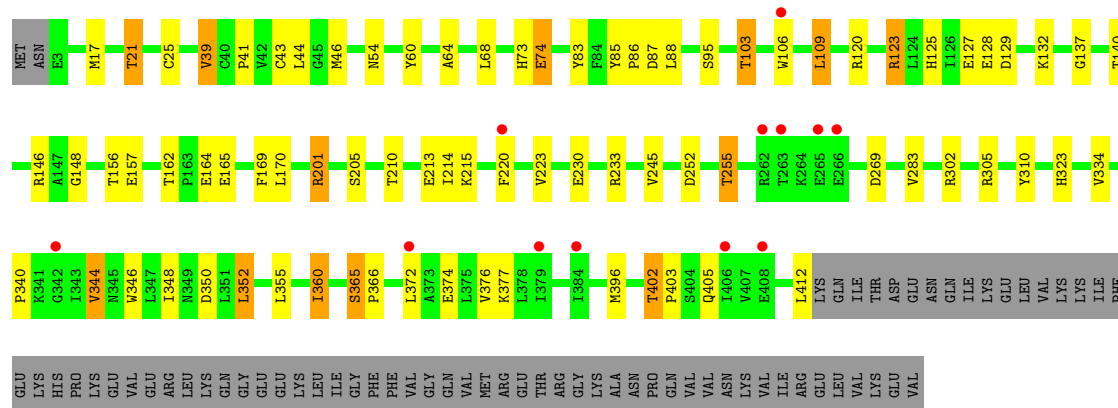
- Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln)amidotransferase subunit B

Chain N:



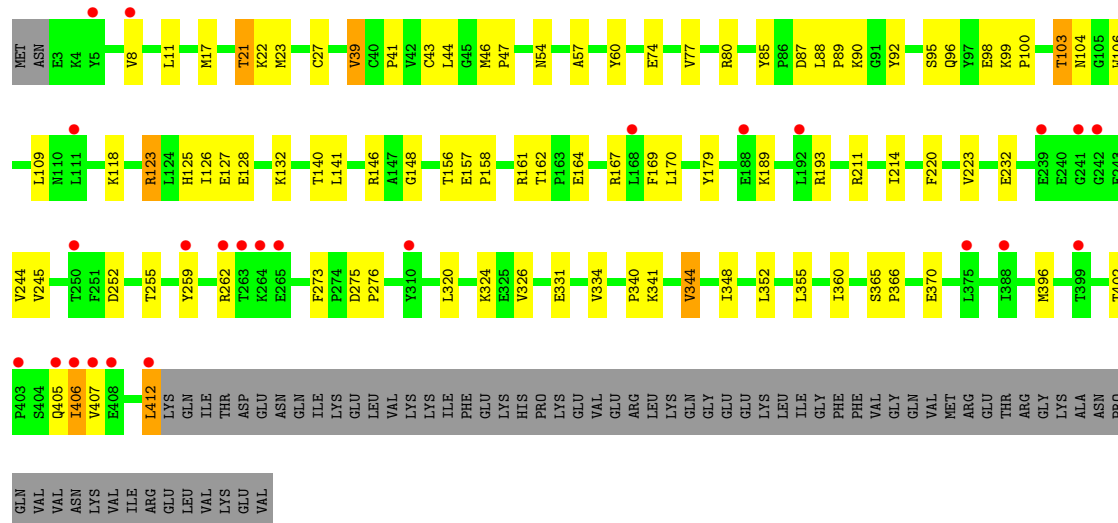
• Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln)amidotransferase subunit B

Chain Q:



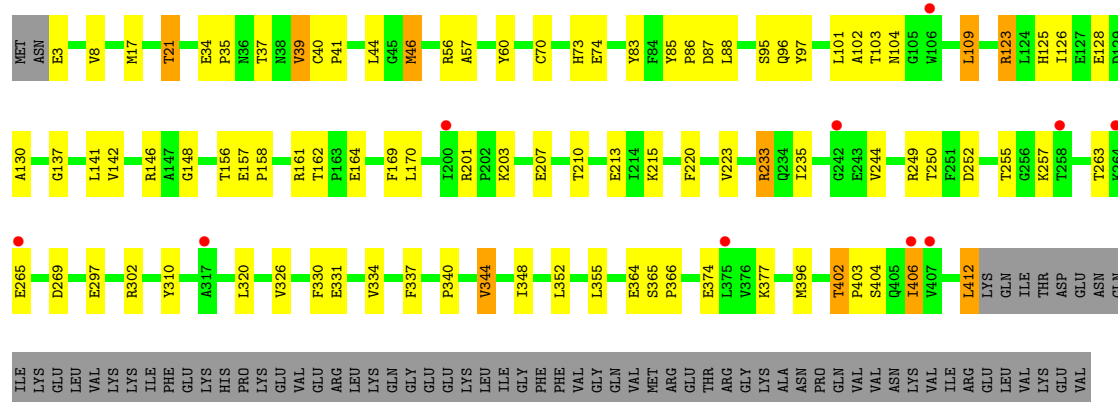
• Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln)amidotransferase subunit B

Chain T:



- Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln)amidotransferase subunit B

Chain W:



- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain C:



- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain F:



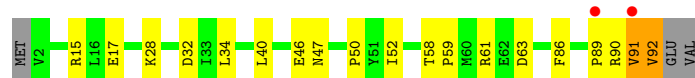
- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain I:



- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain L:



- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain O:



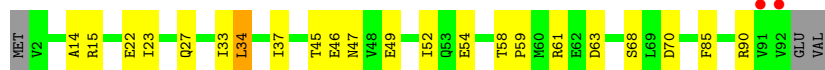
- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain R: 



- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain U: 



- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain X: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	127.48Å 131.01Å 154.67Å 90.02° 90.00° 89.91°	Depositor
Resolution (Å)	40.50 – 2.30 40.51 – 2.30	Depositor EDS
% Data completeness (in resolution range)	91.7 (40.50-2.30) 91.4 (40.51-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.240 , 0.273 0.246 , 0.253	Depositor DCC
R_{free} test set	20322 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	1.104	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 22.4	EDS
Estimated twinning fraction	0.000 for -k,h,l 0.000 for k,-h,l 0.146 for h,-k,-l 0.459 for -h,k,-l 0.146 for -h,-k,l 0.000 for -k,-h,-l 0.000 for k,h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 405875 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	63144	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.50 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.2482e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, ADP

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	0.64	0/3874	0.73	4/5244 (0.1%)
1	D	0.62	0/3874	0.71	0/5244
1	G	0.60	0/3874	0.70	1/5244 (0.0%)
1	J	0.62	1/3874 (0.0%)	0.70	0/5244
1	M	0.59	0/3874	0.69	1/5244 (0.0%)
1	P	0.59	0/3874	0.71	2/5244 (0.0%)
1	S	0.63	0/3874	0.71	0/5244
1	V	0.65	0/3874	0.72	1/5244 (0.0%)
2	B	0.56	0/3371	0.65	1/4541 (0.0%)
2	E	0.62	2/3371 (0.1%)	0.66	1/4541 (0.0%)
2	H	0.57	0/3371	0.66	1/4541 (0.0%)
2	K	0.58	0/3371	0.67	0/4541
2	N	0.57	0/3371	0.67	2/4541 (0.0%)
2	Q	0.56	0/3371	0.69	2/4541 (0.0%)
2	T	0.61	1/3371 (0.0%)	0.66	1/4541 (0.0%)
2	W	0.58	0/3371	0.65	1/4541 (0.0%)
3	C	0.67	0/778	0.72	0/1050
3	F	0.59	0/778	0.69	0/1050
3	I	0.64	0/778	0.66	0/1050
3	L	0.59	0/778	0.69	0/1050
3	O	0.61	0/778	0.67	0/1050
3	R	0.60	0/778	0.69	0/1050
3	U	0.57	0/778	0.65	0/1050
3	X	0.61	0/778	0.70	0/1050
All	All	0.60	4/64184 (0.0%)	0.69	18/86680 (0.0%)

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
2	B	0	2
3	I	0	1
3	O	0	1
3	U	0	1
All	All	0	5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	43	CYS	CB-SG	-5.55	1.72	1.81
2	T	43	CYS	CB-SG	-5.48	1.72	1.81
1	J	84	CYS	CB-SG	-5.26	1.73	1.81
2	E	110	ASN	CG-OD1	5.14	1.35	1.24

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	412	LEU	CA-CB-CG	5.84	128.74	115.30
1	G	117	LEU	CA-CB-CG	5.79	128.60	115.30
1	A	375	ARG	NE-CZ-NH1	5.68	123.14	120.30
2	E	412	LEU	CA-CB-CG	5.67	128.34	115.30
1	P	464	LEU	CA-CB-CG	5.60	128.18	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	39	VAL	Peptide
2	B	97	TYR	Peptide
3	I	45	THR	Peptide
3	O	45	THR	Peptide
3	U	45	THR	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3784	0	3816	92	0
1	D	3784	0	3816	79	0
1	G	3784	0	3816	90	0
1	J	3784	0	3816	70	0
1	M	3784	0	3816	71	0
1	P	3784	0	3816	76	0
1	S	3784	0	3816	91	0
1	V	3784	0	3816	97	0
2	B	3308	0	3354	80	0
2	E	3308	0	3353	72	0
2	H	3308	0	3353	78	0
2	K	3308	0	3353	62	0
2	N	3308	0	3353	65	0
2	Q	3308	0	3353	61	0
2	T	3308	0	3353	72	0
2	W	3308	0	3353	71	0
3	C	764	0	755	11	0
3	F	764	0	755	16	0
3	I	764	0	755	17	0
3	L	764	0	755	21	0
3	O	764	0	755	15	0
3	R	764	0	755	14	0
3	U	764	0	755	15	0
3	X	764	0	755	17	0
4	B	27	0	12	1	0
4	E	27	0	12	0	0
4	H	27	0	12	0	0
4	K	27	0	12	0	0
4	N	27	0	12	0	0
4	Q	27	0	12	0	0
4	T	27	0	12	1	0
4	W	27	0	12	0	0
5	B	1	0	0	0	0
5	E	1	0	0	0	0
5	H	1	0	0	0	0
5	K	1	0	0	0	0
5	N	1	0	0	0	0
5	Q	1	0	0	0	0
5	T	1	0	0	0	0
5	W	1	0	0	0	0
6	B	1	0	0	0	0
6	E	1	0	0	0	0
6	H	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	K	1	0	0	0	0
6	N	1	0	0	0	0
6	Q	1	0	0	0	0
6	T	1	0	0	0	0
6	W	1	0	0	0	0
7	A	8	0	3	1	0
7	D	8	0	3	1	0
7	G	8	0	3	0	0
7	J	8	0	3	0	0
7	M	8	0	3	0	0
7	P	8	0	3	1	0
7	S	8	0	3	1	0
7	V	8	0	3	0	0
All	All	63144	0	63513	1225	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 10.

The worst 5 of 1225 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:190:ARG:HG3	1:A:190:ARG:HH11	1.05	1.16
1:V:77:VAL:HG21	1:V:114:LYS:NZ	1.61	1.13
1:A:47:TYR:O	1:A:51:LEU:HD13	1.54	1.07
1:V:190:ARG:HH11	1:V:190:ARG:HG3	1.10	1.06
1:P:31:ARG:CG	1:P:31:ARG:HH11	1.69	1.05

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	476/478 (100%)	455 (96%)	19 (4%)	2 (0%)	43	52
1	D	476/478 (100%)	456 (96%)	18 (4%)	2 (0%)	43	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	476/478 (100%)	453 (95%)	21 (4%)	2 (0%)	43	52
1	J	476/478 (100%)	457 (96%)	17 (4%)	2 (0%)	43	52
1	M	476/478 (100%)	456 (96%)	18 (4%)	2 (0%)	43	52
1	P	476/478 (100%)	454 (95%)	20 (4%)	2 (0%)	43	52
1	S	476/478 (100%)	454 (95%)	20 (4%)	2 (0%)	43	52
1	V	476/478 (100%)	454 (95%)	20 (4%)	2 (0%)	43	52
2	B	408/478 (85%)	393 (96%)	15 (4%)	0	100	100
2	E	408/478 (85%)	394 (97%)	14 (3%)	0	100	100
2	H	408/478 (85%)	394 (97%)	14 (3%)	0	100	100
2	K	408/478 (85%)	393 (96%)	14 (3%)	1 (0%)	56	68
2	N	408/478 (85%)	394 (97%)	14 (3%)	0	100	100
2	Q	408/478 (85%)	395 (97%)	13 (3%)	0	100	100
2	T	408/478 (85%)	396 (97%)	12 (3%)	0	100	100
2	W	408/478 (85%)	395 (97%)	13 (3%)	0	100	100
3	C	89/94 (95%)	88 (99%)	1 (1%)	0	100	100
3	F	89/94 (95%)	87 (98%)	2 (2%)	0	100	100
3	I	89/94 (95%)	86 (97%)	3 (3%)	0	100	100
3	L	89/94 (95%)	87 (98%)	2 (2%)	0	100	100
3	O	89/94 (95%)	87 (98%)	2 (2%)	0	100	100
3	R	89/94 (95%)	89 (100%)	0	0	100	100
3	U	89/94 (95%)	86 (97%)	3 (3%)	0	100	100
3	X	89/94 (95%)	87 (98%)	2 (2%)	0	100	100
All	All	7784/8400 (93%)	7490 (96%)	277 (4%)	17 (0%)	56	68

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	2	LEU
1	S	2	LEU
1	S	409	GLU
1	G	2	LEU
1	G	65	PHE

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	406/406 (100%)	388 (96%)	18 (4%)	39	51
1	D	406/406 (100%)	383 (94%)	23 (6%)	29	37
1	G	406/406 (100%)	391 (96%)	15 (4%)	45	60
1	J	406/406 (100%)	379 (93%)	27 (7%)	23	29
1	M	406/406 (100%)	385 (95%)	21 (5%)	32	42
1	P	406/406 (100%)	380 (94%)	26 (6%)	25	31
1	S	406/406 (100%)	382 (94%)	24 (6%)	28	35
1	V	406/406 (100%)	388 (96%)	18 (4%)	39	51
2	B	364/427 (85%)	346 (95%)	18 (5%)	35	45
2	E	364/427 (85%)	346 (95%)	18 (5%)	35	45
2	H	364/427 (85%)	346 (95%)	18 (5%)	35	45
2	K	364/427 (85%)	346 (95%)	18 (5%)	35	45
2	N	364/427 (85%)	344 (94%)	20 (6%)	30	39
2	Q	364/427 (85%)	343 (94%)	21 (6%)	28	36
2	T	364/427 (85%)	347 (95%)	17 (5%)	36	47
2	W	364/427 (85%)	348 (96%)	16 (4%)	39	51
3	C	86/89 (97%)	80 (93%)	6 (7%)	21	26
3	F	86/89 (97%)	83 (96%)	3 (4%)	48	63
3	I	86/89 (97%)	81 (94%)	5 (6%)	28	36
3	L	86/89 (97%)	82 (95%)	4 (5%)	36	47
3	O	86/89 (97%)	82 (95%)	4 (5%)	36	47
3	R	86/89 (97%)	82 (95%)	4 (5%)	36	47
3	U	86/89 (97%)	81 (94%)	5 (6%)	28	36
3	X	86/89 (97%)	81 (94%)	5 (6%)	28	36
All	All	6848/7376 (93%)	6494 (95%)	354 (5%)	32	42

5 of 354 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	189	LYS
2	N	103	THR
1	V	279	GLU
2	K	344	VAL
1	M	88	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	205	GLN
1	S	447	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 32 ligands modelled in this entry, 16 are monoatomic - leaving 16 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	$\# Z > 2$
7	ASN	A	901	1	7,7,8	6.46	2 (28%)	6,8,10	1.14	0
4	ADP	B	701	-	29,29,29	1.17	2 (6%)	45,45,45	1.73	6 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	ASN	D	902	1	7,7,8	6.95	1 (14%)	6,8,10	1.17	1 (16%)
4	ADP	E	702	-	29,29,29	1.08	2 (6%)	45,45,45	1.76	8 (17%)
7	ASN	G	903	1	7,7,8	6.74	3 (42%)	6,8,10	2.28	3 (50%)
4	ADP	H	703	-	29,29,29	1.25	4 (13%)	45,45,45	1.57	5 (11%)
7	ASN	J	904	1	7,7,8	6.46	2 (28%)	6,8,10	1.25	0
4	ADP	K	704	-	29,29,29	1.15	2 (6%)	45,45,45	1.80	8 (17%)
7	ASN	M	905	1	7,7,8	7.25	2 (28%)	6,8,10	1.55	1 (16%)
4	ADP	N	705	-	29,29,29	1.29	4 (13%)	45,45,45	1.61	6 (13%)
7	ASN	P	906	1	7,7,8	6.36	1 (14%)	6,8,10	1.54	1 (16%)
4	ADP	Q	706	-	29,29,29	1.09	2 (6%)	45,45,45	1.69	7 (15%)
7	ASN	S	907	1	7,7,8	6.98	4 (57%)	6,8,10	1.77	1 (16%)
4	ADP	T	707	-	29,29,29	1.12	2 (6%)	45,45,45	1.66	8 (17%)
7	ASN	V	908	1	7,7,8	6.34	3 (42%)	6,8,10	0.92	0
4	ADP	W	708	-	29,29,29	1.07	2 (6%)	45,45,45	1.70	7 (15%)

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
7	ASN	A	901	1	-	0/6/7/8	0/0/0/0
4	ADP	B	701	-	-	0/16/32/32	0/1/3/3
7	ASN	D	902	1	-	0/6/7/8	0/0/0/0
4	ADP	E	702	-	-	0/16/32/32	0/1/3/3
7	ASN	G	903	1	-	0/6/7/8	0/0/0/0
4	ADP	H	703	-	-	0/16/32/32	0/1/3/3
7	ASN	J	904	1	-	0/6/7/8	0/0/0/0
4	ADP	K	704	-	-	0/16/32/32	0/1/3/3
7	ASN	M	905	1	-	0/6/7/8	0/0/0/0
4	ADP	N	705	-	-	0/16/32/32	0/1/3/3
7	ASN	P	906	1	-	0/6/7/8	0/0/0/0
4	ADP	Q	706	-	-	0/16/32/32	0/1/3/3
7	ASN	S	907	1	-	0/6/7/8	0/0/0/0
4	ADP	T	707	-	-	0/16/32/32	0/1/3/3
7	ASN	V	908	1	-	0/6/7/8	0/0/0/0
4	ADP	W	708	-	-	0/16/32/32	0/1/3/3

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	M	905	ASN	OD1-CG	18.89	1.24	1.11
7	D	902	ASN	OD1-CG	18.12	1.23	1.11
7	S	907	ASN	OD1-CG	17.92	1.23	1.11
7	G	903	ASN	OD1-CG	17.43	1.23	1.11
7	J	904	ASN	OD1-CG	16.69	1.22	1.11

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	704	ADP	N3-C2-N1	-6.61	123.19	128.71
4	E	702	ADP	N3-C2-N1	-6.28	123.45	128.71
4	H	703	ADP	N3-C2-N1	-6.06	123.64	128.71
4	N	705	ADP	N3-C2-N1	-5.78	123.88	128.71
4	B	701	ADP	N3-C2-N1	-5.75	123.90	128.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

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	478/478 (100%)	0.07	9 (1%) 64 73	23, 44, 71, 79	0
1	D	478/478 (100%)	-0.01	6 (1%) 74 82	29, 44, 71, 80	0
1	G	478/478 (100%)	0.09	2 (0%) 90 95	29, 43, 71, 79	0
1	J	478/478 (100%)	0.09	4 (0%) 83 90	28, 43, 71, 79	0
1	M	478/478 (100%)	0.03	2 (0%) 90 95	29, 43, 71, 79	0
1	P	478/478 (100%)	0.10	2 (0%) 90 95	28, 43, 71, 79	0
1	S	478/478 (100%)	0.03	6 (1%) 74 82	29, 44, 71, 79	0
1	V	478/478 (100%)	0.03	5 (1%) 79 87	29, 44, 71, 79	0
2	B	410/478 (85%)	0.22	9 (2%) 59 69	28, 54, 85, 103	0
2	E	410/478 (85%)	0.30	28 (6%) 17 25	29, 54, 85, 103	0
2	H	410/478 (85%)	0.28	17 (4%) 35 46	29, 54, 85, 103	0
2	K	410/478 (85%)	0.35	17 (4%) 35 46	29, 54, 85, 103	0
2	N	410/478 (85%)	0.27	11 (2%) 52 62	29, 54, 85, 103	0
2	Q	410/478 (85%)	0.32	12 (2%) 49 59	28, 54, 85, 103	0
2	T	410/478 (85%)	0.32	25 (6%) 21 29	28, 54, 85, 103	0
2	W	410/478 (85%)	0.26	10 (2%) 56 66	29, 54, 85, 103	0
3	C	91/94 (96%)	0.24	1 (1%) 77 85	39, 50, 64, 68	0
3	F	91/94 (96%)	0.16	1 (1%) 77 85	39, 50, 64, 67	0
3	I	91/94 (96%)	0.16	1 (1%) 77 85	39, 50, 64, 68	0
3	L	91/94 (96%)	0.26	2 (2%) 59 69	39, 50, 64, 67	0
3	O	91/94 (96%)	0.21	1 (1%) 77 85	39, 50, 64, 68	0
3	R	91/94 (96%)	0.28	0 100 100	39, 50, 64, 67	0
3	U	91/94 (96%)	0.11	2 (2%) 59 69	39, 50, 64, 68	0
3	X	91/94 (96%)	0.20	2 (2%) 59 69	39, 50, 64, 68	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
All	All	7832/8400 (93%)	0.17	175 (2%)	59	69	23, 47, 79, 103	0

The worst 5 of 175 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	T	242	GLY	6.4
2	T	412	LEU	5.7
2	H	262	ARG	5.2
2	N	408	GLU	5.2
2	W	406	ILE	5.2

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 carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	MG	B	801	1/1	0.19	7.71	10,10,10,10	0
5	MG	Q	806	1/1	0.18	4.49	21,21,21,21	0
5	MG	W	808	1/1	0.17	3.45	18,18,18,18	0
5	MG	T	807	1/1	0.18	3.30	15,15,15,15	0
5	MG	N	805	1/1	0.20	2.88	16,16,16,16	0
7	ASN	M	905	8/9	0.17	2.15	32,33,34,36	0
5	MG	H	803	1/1	0.19	2.00	10,10,10,10	0
6	ZN	B	901	1/1	0.16	1.81	37,37,37,37	0
7	ASN	D	902	8/9	0.13	1.16	39,40,40,41	0
5	MG	K	804	1/1	0.16	1.13	11,11,11,11	0
6	ZN	T	907	1/1	0.14	1.11	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	ZN	H	903	1/1	0.15	1.11	33,33,33,33	0
4	ADP	H	703	27/27	0.16	1.03	44,48,63,65	27
5	MG	E	802	1/1	0.14	0.98	19,19,19,19	0
7	ASN	A	901	8/9	0.14	0.77	33,33,36,36	0
6	ZN	Q	906	1/1	0.15	0.68	30,30,30,30	0
6	ZN	W	908	1/1	0.14	0.56	33,33,33,33	0
6	ZN	N	905	1/1	0.14	0.30	36,36,36,36	0
7	ASN	G	903	8/9	0.12	0.27	28,30,31,31	0
4	ADP	W	708	27/27	0.15	0.19	48,50,68,70	27
6	ZN	K	904	1/1	0.13	0.19	29,29,29,29	0
7	ASN	P	906	8/9	0.13	0.04	28,32,33,34	0
4	ADP	N	705	27/27	0.16	0.03	49,52,63,65	27
4	ADP	B	701	27/27	0.14	-0.00	46,49,65,66	27
7	ASN	V	908	8/9	0.10	-0.05	29,30,31,32	0
4	ADP	E	702	27/27	0.15	-0.05	59,60,72,73	27
4	ADP	T	707	27/27	0.14	-0.08	51,52,70,71	27
7	ASN	S	907	8/9	0.10	-0.40	28,32,33,33	0
6	ZN	E	902	1/1	0.10	-0.46	40,40,40,40	0
4	ADP	Q	706	27/27	0.15	-0.47	44,46,65,66	27
4	ADP	K	704	27/27	0.14	-0.79	40,41,64,66	27
7	ASN	J	904	8/9	0.11	-1.12	26,28,29,29	0

6.5 Other polymers ⓘ

There are no such residues in this entry.